MOLECULAR SEQUENCE OF SWINE RETROVIRUS AND METHODS OF USE
Jay A. Fishman
14846-011004

CTCGAGACTC GGTGGAAGGG CCCTTATCTC GTACTTTTGA CCACACCAAC   50   (SEQ ID NO: 1)

GGCTGTGAAA GTCGAAGGAA TCTCCACCTG GATCCATGCA TCCCACGTTA   100

AGCCGGCGCC ACCTCCCGAT TCGGGGTGGA AAGCCGAAAA GACTGAAAAT   150

CCCCTTAAGC TTCGCCTCCA TCGCGTGGTT CCTTACTCTG TCAATAACCT   200

CTCAGACTAA TGGTATGCGC ATAGGAGACA GCCTGAACTC CCATAAACCC   250

TTATCTCTCA CCTGGTTAAT TACTGACTCC GGCACAGGTA TTAATATCAA   300

CAACACTCAA GGGGAGGCTC CTTTAGGAAC CTGGTGGCCT GATCTATACG   .350

TTTGCCTCAG ATCAGTTATT CCTAGTCTGA CCTCACCCCC AGATATCCTC   400

CATGCTCACG GATTTTATGT TTGCCCAGGA CCACCAAATA ATGGAAAACA   450

TTGCGGAAAT CCCAGAGATT TCTTTTGTAA ACAATGGAAC TGTGTAACCT   500

CTAATGATGG ATATTGGAAA TGGCCAACCT CTCAGCAGGA TAGGGTAAGT   550

TTTTCTTATG TCAACACCTA TACCAGCTCT GGACAATTTA ATTACCTGAC   600

CTGGATTAGA ACTGGAAGCC CCAAGTGCTC TCCTTCAGAC CTAGATTACC   650

TAAAAATAAG TTTCACTGAG AAAGGAAAAC AAGAAAATAT CCTAAAAATGG   700

GTAAATGGTA TGTCTTGGGG AATGGTATAT TATGGAGGCT CGGGTAAACA   750

ACCAGGCTCC ATTCTAACTA TTCGCCTCAA AATAAACCAG CTGGAGCCTC   800

CAATGGCTAT AGGACCAAAT ACGGTCTTGA CGGGTCAAAG ACCCCCAACC   850

CAAGGACCAG GACCATCCTC TAACATAACT TCTGGATCAG ACCCCACTGA   900

GTCTAGCAGC ACGACTAAAA TGGGGGCAAA ACTTTTTAGC CTCATCCAGG   950

GAGCTTTTCA AGCTCTTAAC TCCACGACTC CAGAGGCTAC CTCTTCTTGT   1000

TGGCTATGCT TAGCTTTGGG CCCACCTTAC TATGAAGGAA TGGCTAGAAG   1050

AGGGAAATTC AATGTGACAA AAGAACATAG AGACCAATGC ACATGGGGAT   1100

CCCAAAATAA GCTTACCCTT ACTGAGGTTT CTGGAAAAGG CACCTGCATA   1150

GGAAAGGTTC CCCCATCCCA CCAACACCTT TGTAACCACA CTGAAGCCTT   1200

TAATCAAACC TCTGAAAGTC AATATCTGGT ACCTGGTTAT GACAGGTGGT   1250

TGTAA TACTGGATTA ACCCCTTGTG TTTCCACCTT GGTTTTTAAC   1300

FIGURE 1

CAAACTAAAG ATTTTTGCAT TATGGTCCAA ATTGTTCCCC GAGTGTATTA   1350   (SEQ ID NO: 1) cont'd

CTATCCCGAA AAAGCAATCC TTGATGAATA TGACTACAGA AATCATCGAC   1400

AAAAGAGAGA ACCCATATCT CTGACACTTG CTGTGATGCT CGGACTTGGA   1450

GTGGCAGCAG GTGTAGGAAC AGGAACAGCT GCCCTGGTCA CGGGACCACA   1500

GCAGCTAGAA ACAGGACTTA GTAACCTACA TCGAATTGTA ACAGAAGATC   1550

TCCAAGCCCT AGAAAAATCT GTCAGTAACC TGGAGGAATC CCTAACCTCC   1600

TTATCTGAAG TAGTCCTACA GAATAGAAGA GGGTTAGATT TATTATTTCT   1650

AAAAGAAGGA GGATTATGTG TAGCCTTGAA GGAGGAATGC TGTTTTTATG   1700

TGGATCATTC AGGGGCCATC AGAGACTCCA TGAACAAACT TAGAGAAAGG   1750

TTGGAGAAGC GTCGAAGGGA AAAGGAAACT ACTCAAGGGT GGTTTGAGGG   1800

ATGGTTCAAC AGGTCTCCTT GGTTGGCTAC CCTACTTTCT GCTTTAACAG   1850

GACCCTTAAT AGTCCTCCTC CTGTTACTCA CAGTTGGGCC ATGTATTATT   1900

AACAAGTTAA TTGCCTTCAT TAGAGAACGA ATAAGTGCAG TCCAGATCAT   1950

GGTACTTAGA CAACAGTACC AAAGCCCGTC TAGCAGGGAA GCTGGCCGCT   2000

AGCTCTACCA GTTCTAAGAT TAGAACTATT AACAAGAGAA GAAGTGGGGA   2050

ATGAAAGGAT GAAAATACAA CCTAAGCTAA TGAGAAGCTT AAAATTGTTC   2100

TGAATTCCAG AGTTTGTTCC TTATAGGTAA AAGATTAGGT TTTTTGCTGT   2150

TTTAAAATAT GCGGAAGTAA AATAGGCCCT GAGTACATGT CTCTAGGCAT   2200

GAAACTTCTT GAAACTATTT GAGATAACAA GAAAAGGGAG TTTCTAACTG   2250

CTTGTTTAGC TTCTGTAAAA CTGGTTGCGC CATAAAGATG TTGAAATGTT   2300

GATACACATA TCTTGGTGAC AACATGTCTC CCCCACCCCG AAACATGCGC   2350

AAATGTGTAA CTCTAAAACA ATTTAAATTA ATTGGTCCAC GAAGCGCGGG   2400

CTCTCGAAGT TTTAAATTGA CTGGTTTGTG ATATTTTGAA ATGATTGGTT   2450

TGTAAAGCGC GGGCTTTGCT GTGAACCCCA TAAAAGCTGT CCCGACTCCA   2500

CACTCGGGGC CGCAGTCCTC TACCCCTGCG TGGTGTACGA CTGTGGGCCC   2550

FIGURE 1, CONT.

CAGCGCGCTT GGAATAAAAA TCCTCTTGCT GTTTGCATCA AGACCGCTTC   2600   (SEQ ID NO: 1) cont'd

TCGTGAGTGA TTAAGGGGAG TCGCCTTTTC CGAGCCTGGA GGTTCTTTTT   2650

GCTGGTCTTA CATTTGGGGG CTCGTCCGGG ATCTGTCGCG GCCACCCCTA   2700

ACACCCGAGA ACCGACTTGG AGGTAAAAAG GATCCTCTTT TTAACGTGTA   2750

TGCATGTACC GGCCGGCGTC TCTGTTCTGA GTGTCTGTTT TCAGTGGTGC   2800

GCGCTTTCGG TTTGCAGCTG TCCTCTCAGG CCGTAAGGGC TGGGGGACTG   2850

TGATCAGCAG ACGTGCTAGG AGGATCACAG GCTGCTGCCC TGGGGGACGC   2900

CCCGGGAGGT GAGGAGAGCC AGGGACGCCT GGTGGTCTCC TACTGTCGGT   2950

CAGAGGACCG AATTCTGTTG CTGAAGCGAA AGCTTCCCCC TCCGCGACCG   3000

TCCGACTCTT TTGCCTGCTT GTGGAATACG TGGACGGGTC ACGTGTGTCT   3050

GGATCTGTTG GTTTCTGTTT TGTGTGTCTT TGTCTTGTGT GTCCTTGTCT   3100

ACAGTTTTAA TATGGGACAG ACGGTGACGA CCCCTCTTAG TTTGACTCTC   3150

GACCATTGGA CTGAAGTTAA ATCCAGGGCT CATAATTTGT CAGTTCAGGT   3200

TAAGAAGGGA CCTTGGCAGA CTTTCTGTGT CTCTGAATGG CCGACATTCG   3250

ATGTTGGATG GCCATCAGAG GGGACCTTTA ATTCTGAGAT TATCCTGGCT   3300

GTTAAAGCAA TTATTTTTCA GACTGGACCC GGCTCTCATC CCGATCAGGA   3350

GCCCTATATC CTTACGTGGC AAGATTTGGC AGAGGATCCT CCGCCATGGG   3400

TTAAACCATG GCTGAATAAG CCAAGAAAGC CAGGTCCCCG AATTCTGGCT   3450

CTTGGAGAGA AAAACAAACA CTCGGCTGAA AAAGTCAAGC CCTCTCCTCA   3500

TATCTACCCC GAGATTGAGG AACCACCGGC TTGGCCGGAA CCCCAATCTG   3550

TTCCCCCACC CCCTTATCTG GCACAGGGTG CCGCGAGGGG ACCCTTTGCC   3600

CCTCCTGGAG CTCCGGCGGT GGAGGGACCT TCTGCAGGGA CTCGGAGCCG   3650

GAGGGGCGCC ACCCCGGAGC GGACAGACGA GATCGCGACA TTACCGCTGC   3700

GCACGTACGG CCCTCCCACA CCGGGGGGCC AATTGCAGCC CCTCCAGTAT   3750

TGGCCCTTTT CTTCTGCAGA TCTCTATAAT TGGAAAACTA ACCATCCCCC   3800

FIGURE 1, CONT.

TTTCTCGGAG GATCCCCAAC GCCTCACGGG GTTGGTGGAG TCCCTTATGT   3850   (SEQ ID NO: 1) cont'd

TCTCTCACCA GCCTACTTGG GATGATTGTC AACAGCTGCT GCAGACACTC   3900

TTCACAACCG AGGAGCGAGA GAGAATTCTA TTAGAGGCTA GAAAAAATGT   3950

TCCTGGGGCC GACGGGCGAC CCACGCGGTT GCAAAATGAG ATTGACATGG   4000

GATTTCCCTT AACTCGCCCC GGTTGGGACT ACAACACGGC TGAAGGTAGG   4050

GAGAGCTTGA AAATCTATCG CCAGGCTCTG GTGGCGGGTC TCCGGGGCGC   4100

CTCAAGACGG CCCACTAATT TGGCTAAGGT AAGAGAAGTG ATGCAGGGAC   4150

CGAATGAACC CCCCTCTGTT TTTCTTGAGA GGCTCTTGGA AGCCTTCAGG   4200

CGGTACACCC CTTTTGATCC CACCTCAGAG GCCCAAAAAG CCTCAGTGGC   4250

TTTGGCCTTT ATAGGACAGT CAGCCTTGGA TATTAGAAAG AAGCTTCAGA   4300

GACTGGAAGG GTTACAGGAG GCTGAGTTAC GTGATCTAGT GAAGGAGGCA   4350

GAGAAAGTAT ATTACAAAAG GGAGACAGAA GAAGAAAGGG AACAAAGAAA   4400

AGAGAGAGAA AGAGAGGAAA GGGAGGAAAG ACGTAATAAA CGGCAAGAGA   4450

AGAATTTGAC TAAGATCTTG GCTGCAGTGG TTGAAGGGAA AAGCAATACG   4500

GAAAGAGAGA GAGATTTTAG GAAAATTAGG TCAGGCCCTA GACAGTCAGG   4550

GAACCTGGGC AATAGGACCC CACTCGACAA GGACCAATGT GCATATTGTA   4600

AAGAAAGAGG ACACTGGGCA AGGAACTGCC CCAAGAAGGG AAACAAAGGA   4650

CCAAGGATCC TAGCTCTAGA AGAAGATAAA GATTAGGGGA GACGGGGTTC   4700

GGACCCCCTC CCCGAGCCCA GGGTAACTTT GAAGGTGGAG GGGCAACCAG   4750

TTGAGTTCCT GGTTGATACC GGAGCGAAAC ATTCAGTGCT ACTACAGCCA   4800

TTAGGAAAAC TAAAAGATAA AAAATCCTGG GTGATGGGTG CACAGGGCAA   4850

CAACAGTATC CATGGACTAC CCGAAGACAG TTGACTTGGG AGTGGGACGG   4900

GTAACCCACT CGTTTCTGGT CATACCTGAG TGCCCAGCAC CCCTCTTAGG   4950

TAGAGACTTA TTGACCAAGA TGGGAGCACA AATTTCTTTT GAACAAGGGA   5000

AACCAGAAGT GTCTGCAAAT AACAAACCTA TCACTGTGTT GACCCTCCAA   5050

FIGURE 1, CONT.

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TTAGATGACG AATATCGACT ATACTCTCCC CTAGTAAAGC CTGATCAAAA   5100   (SEQ ID NO: 1) cont'd

TATACAATTC TGGTTGGAAC AGTTTCCCCA AGCCTGGGCA GAAACCGCAG   5150

GGATGGGTTT GGCAAAGCAA GTTCCCCCAC AAGTTATTCA ACTGAAGGCC   5200

AGTGCCACAC CAGTGTCAGT CAGACAGTAC CCCTTGAGTA AAGAAGCTCA   5250

AGAAGGAATT CGGCCGCATG TCCAAAGATT AATCCAACAG GGCATCCTAG   5300

TTCCTGTCCA ATCTCCCTGG AATACTCCCC TGCTACCGGT TAGAAAGCCT   5350

GGGACTAATG ACTATCGACC AGTACAGGAC TTGAGAGAGG TCAATAAACG   5400

GGTGCAGGAT ATACACCCAA CAGTCCCGAA CCCTTATAAC CTCTTGTGTG   5450

CTCTCCCACC CCAACGGAGC TGGTATACAG TATTGGACTT AAAGGATGCC   5500

TTCTTCTGCC TGAGATTACA CCCCACTAGC CAACCACTTT TTGCCTTCGA   5550

ATGGAGAGAT CCAGGTACGG GAAGAACCGG GCAGCTCACC TGGACCCGAC   5600

TGCCCCAAGG GTTCAAGAAC TCCCCGACCA TCTTTGACGA AGCCCTACAC   5650

AGAGACCTGG CCAACTTCAG GATCCAACAC CCTCAGGTGA CCCTCCTCCA   5700

GTACGTGGAT GACCTGCTTC TGGCGGGAGC CACCAAACAG GACTGCTTAG   5750

AAGGCACGAA GGCACTACTG CTGGAATTGT CTGACCTAGG CTACAGAGCC   5800

TCTGCTAAGA AGGCCCAGAT TTGCAGGAGA GAGGTAACAT ACTTGGGGTA   5850

CAGTTTACGG GACGGGCAGC GATGGCTGAC GGAGGCACGG AAGAAAACTG   5900

TAGTCCAGAT ACCGGCCCCA ACCACAGCCA AACAAATGAG AGAGTTTTTG   5950

GGGACAGCTG GATTTTGCAG ACTGTGGATC CCGGGGTTTG CGACCTTAGC   6000

AGCCCCACTC TACCCGCTAA CCAAAGAAAA AGGGGAATTC TCCTGGGCTC   6050

CTGAGCACCA GAAGGCATTT GATGCTATCA AAAAGGCCCT GCTGAGCGCA   6100

CCTGCTCTGG CCCTCCCTGA CGTAACTAAA CCCTTTACCC TTTATGTGGA   6150

TGAGCGTAAG GGAGTAGCCC GGGGAGTTTT AACCCAAACC CTAGGACCAT   6200

GGAGAAGACC TGTCGCCTAC CTGTCAAAGA AGCTCGATCC TGTAGCCAGT   6250

GGTTGGCCCA TATGCCTGAA GGCTATCGCA GCTGTGGCCA TACTGGTCAA   6300

FIGURE 1, CONT.

GGACGCTGAC AAATTGACTT TGGGACAAGA ATATAACTGT AATAGCCCCC   6350   (SEQ ID NO: 1) cont'd

CATGCATTGG AGAACATCGT TCGGCAGCCC CCAGACCGAT GGATGACCAA   6400

CGCCCGCATG ACCCACTATC AAAGCCTGCT TCTCACAGAG AGGGTCACGT   6450

TCGCTCCACC AACCGCTCTC AACCCTGCCA CTCTTCTGCC TGAAGAGACT   6500

GATGAACCAG TGACTCATGA TTGCCATCAA CTATTGATTG AGGAGACTGG   6550

GGTCCGCAAG GACCTTACAG ACATACCGCT GACTGGAGAA GTGCTAACCT   6600

GGTTCACTGA CGGAAGCAGC TATGTGGTGG AAGGTAAGAG GATGGCTGGG   6650

GCGGCGGTGG TGGACGGGAC CCGCACGATC TGGGCCAGCA GCCTGCCGGG   6700

AGGAACTTCA GCACAAAAGG CTGAGCTCAT GGCCCTCACG CAAGCTTTGC   6750

GGCTGGCCGA AGGGAAATCC ATAAACATTT ATACGGACAG CAGGTATGCC   6800

TTTGCGACTG CACACGTACA TGGGGCCATC TATAAACAAA GGGGGTTGCT   6850

TACCTCAGCA GGGAGGGAAA TAAAGAACAA AGAGGAAATT CTAAGCCTAT   6900

TAGAAGCCGT ACATTTACCA AAAAGGCTAG CTATTATACA CTGTCCTGGA   6950

CATCAGAAAG CTAAAGATCT CATATCCAGA GGAAACCAGA TGGCTGACCG   7000

GGTTGCCAAG CAGGCAGCCC AGGGTGTTAA CCTTCTGCCT ATAATAGAAA   7050

TGCCCAAAGC CCCAGAACCC AGACGACAGT ACACCCTAGA AGACTGGCAA   7100

GAGATAAAAA AGATAGACCA TTCTCTGAGA CTCCGGAAGG GACCTGCTAT   7150

ACCTCAGATG GGAAGGAAAT CCTGCCCCAC AAAGAAGGGT TAGAATATGT   7200

CCAACAAGAT ACATCGTCTA ACCCACCTAG GAACTAAACA CCTGCAGCAG   7250

TTGGTCAGAA CATCCCCTTA TCATGTTCTG AGGCTACCAG GAGTGGCTGA   7300

CTCGGTGGTC AAACATTGTG TGCCCTGCCA GCTGGTTAAT GCTAATCCTT   7350

CCAGAATGCC TCCAGGGAAG AGACTAAGGG GAAGCCACCC AGGCGCTCAC   7400

TGGGAAGTGG ACTTCACTGA GGTAAAGCCG GCTAAATATG GAAACAAATA   7450

CCTATTGGTT TTTGTAGACA CCTTTTCAGG ATGGGTAGAG GCTTATCCTA   7500

CTAAGAAAGA GACTTCAACC GTGGTAGCTA AAAAAATACT GGAAGAAATT   7550

FIGURE 1, CONT.

TTTCCAAGAT TTGGAATACC TAAGGTAATA GGGTCAGACA ATGGTCCAGC   7600   (SEQ ID NO: 1) cont'd

TTTTGTTGCC CAGGTAAGTC AGGGACTGGC CAAGATATTG GGGATTGATT   7650

GGAAACTGCA TTGTGCATAC AGACCCCAAA GCTCAGGACA GGTAGAGAGG   7700

ATGAATAGAA CCATTAAAGA GACCCTTACT AAATTGACCG CGGAGACTGG   7750

CGTTAATGAT TGGATAGCTC TCCTGCCCTT TGTGCTTTTT AGGGTTAGGA   7800

ACACCCCTGG ACAGTTTGGG CTGACCCCCT ATGAATTACT CTACGGGGGA   7850

CCCCCCCCAT TGGTAGAAAT TGCTTCTGTA CATAGTGCTG ATGTGCTGCT   7900

TTCCCAGCCT TTGTTCTCTA GGCTCAAGGC ACTTGAGTGG GTGAGACAAC   7950

GAGCGTGGAG GCAACTCCGG GAGGCCTACT CAGGAGGAGG AGACTTGCAG   8000

ATCCCACATC GTTTCCAAGT GGGAGATTCA GTCTACGTTA GACGCCACCG   8050

TGCAGGAAAC   8060

FIGURE 1, CONT.

(SEQ ID NO: 2)

```
        10        20        30        40        50        60
    *    *    *    *    *    *    *    *    *    *    *    *
CTACCCCTGC GTGGTGTACG ACTGTGGGCC CCAGCGCGCT TGGAATAAAA ATCCTCTTGC

        70        80        90       100       110       120
    *    *    *    *    *    *    *    *    *    *    *    *
TGTTTGCATC AAGACCGCTT CTTGTGAGTG ATTTGGGGTG TCGCCTCTTC CGAGCCCGGA

       130       140       150       160       170       180
    *    *    *    *    *    *    *    *    *    *    *    *
CGAGGGGGAT TGTTCTTTTA CTGGCCTTTC ATTTGGTGCG TTGGCCGGGA AATCCTGCGA

       190       200       210       220       230       240
    *    *    *    *    *    *    *    *    *    *    *    *
CCACCCCTTA CACCCGAGAA CCGACTTGGA GGTAAAGGGA TCCCCTTTGG AACATATGTG

       250       260       270       280       290       300
    *    *    *    *    *    *    *    *    *    *    *    *
TGTGTCGGCC GGCGTCTCTG TTCTGAGTGT CTGTTTTCGG TGATGCGCGC TTTCGGTTTG

       310       320       330       340       350       360
    *    *    *    *    *    *    *    *    *    *    *    *
CAGCTGTCCT CTCAGACCGT AAGGACTGGA GGACTGTGAT CAGCAGACGT GCTAGGAGGA

       370       380       390       400       410       420
    *    *    *    *    *    *    *    *    *    *    *    *
TCACAGGCTG CCACCCTGGG GGACGCCCCG GGAGGTGGGG AGAGCCAGGG ACGCCTGGTG

       430       440       450       460       470       480
    *    *    *    *    *    *    *    *    *    *    *    *
GTCTCCTACT GTCGGTCAGA GGACCGAGTT CTGTTGTTGA AGCGAAAGCT TCCCCCTCCG

       490       500       510       520       530       540
    *    *    *    *    *    *    *    *    *    *    *    *
CGGCCGTCCG ACTCTTTTGC CTGCTTGTGG AAGACGCGGA CGGGTCGCGT GTGTCTGGAT

       550       560       570       580       590       600
    *    *    *    *    *    *    *    *    *    *    *    *
CTGTTGGTTT CTGTTTCGTG TGTCTTTGTC TTGTGCGTCC TTGTCTACAG TTTTTAAT ATG
                                                          Met>
```

```
          610       620       630       640
      *     *    *    *    *    *    *    *    *
GGA CAG ACA GTG ACT ACC CCC CTT AGT TTG ACT CTC GAC CAT TGG ACT
Gly Gln Thr Val Thr Thr Pro Leu Ser Leu Thr Leu Asp His Trp Thr>

650       660       670       680       690
  *    *    *    *    *    *    *    *    *    *
GAA GTT AGA TCC AGG GCT CAT AAT TTG TCA GTT CAG GTT AAG AAG GGA
Glu Val Arg Ser Arg Ala His Asn Leu Ser Val Gln Val Lys Lys Gly>

   700       710       720       730       740
    *    *    *    *    *    *    *    *    *    *
CCT TGG CAG ACT TTC TGT GCC TCT GAA TGG CCA ACA TTC GAT GTT GGA
Pro Trp Gln Thr Phe Cys Ala Ser Glu Trp Pro Thr Phe Asp Val Gly>
```

FIGURE 2

```
              750          760          770          780          790
      *     *      *      *      *      *      *      *      *      *              (SEQ ID NO: 2) cont'd
    TGG CCA TCA GAG GGG ACC TTT AAT TCT GAA ATT ATC CTG GCT GTT AAG
    Trp Pro Ser Glu Gly Thr Phe Asn Ser Glu Ile Ile Leu Ala Val Lys>

                800          810          820          830          840
      *      *      *      *      *      *      *      *      *      *
    GCA ATC ATT TTT CAG ACT GGA CCC GGC TCT CAT CCT GAT CAG GAG CCC
    Ala Ile Ile Phe Gln Thr Gly Pro Gly Ser His Pro Asp Gln Glu Pro>

                850          860          870          880
      *      *      *      *      *      *      *      *      *
    TAT ATC CTT ACG TGG CAA GAT TTG GCA GAA GAT CCT CCG CCA TGG GTT
    Tyr Ile Leu Thr Trp Gln Asp Leu Ala Glu Asp Pro Pro Pro Trp Val>

    890          900          910          920          930
      *      *      *      *      *      *      *      *      *      *
    AAA CCA TGG CTA AAT AAA CCA AGA AAG CCA GGT CCC CGA ATC CTG GCT
    Lys Pro Trp Leu Asn Lys Pro Arg Lys Pro Gly Pro Arg Ile Leu Ala>

        940          950          960          970          980
      *      *      *      *      *      *      *      *      *
    CTT GGA GAG AAA AAC AAA CAC TCG GCC GAA AAA GTC GAG CCC TCT CCT
    Leu Gly Glu Lys Asn Lys His Ser Ala Glu Lys Val Glu Pro Ser Pro>

        990         1000         1010         1020         1030
      *      *      *      *      *      *      *      *      *      *
    CGT ATC TAC CCC GAG ATC GAG GAG CCG CCG ACT TGG CCG GAA CCC CAA
    Arg Ile Tyr Pro Glu Ile Glu Glu Pro Pro Thr Trp Pro Glu Pro Gln>

            1040         1050         1060         1070         1080
      *      *      *      *      *      *      *      *      *      *
    CCT GTT CCC CCA CCC CCT TAT CCA GCA CAG GGT GCT GTG AGG GGA CCC
    Pro Val Pro Pro Pro Pro Tyr Pro Ala Gln Gly Ala Val Arg Gly Pro>

            1090         1100         1110         1120
      *      *      *      *      *      *      *      *      *
    TCT GCC CCT CCT GGA GCT CCG GTG GTG GAG GGA CCT GCT GCC GGG ACT
    Ser Ala Pro Pro Gly Ala Pro Val Val Glu Gly Pro Ala Ala Gly Thr>

    1130         1140         1150         1160         1170
      *      *      *      *      *      *      *      *      *      *
    CGG AGC CGG AGA GGC GCC ACC CCG GAG CGG ACA GAC GAG ATC GCG ATA
    Arg Ser Arg Arg Gly Ala Thr Pro Glu Arg Thr Asp Glu Ile Ala Ile>

        1180         1190         1200         1210         1220
      *      *      *      *      *      *      *      *      *      *
    TTA CCG CTG CGC ACC TAT GGC CCT CCC ATG CCA GGG GGC CAA TTG CAG
    Leu Pro Leu Arg Thr Tyr Gly Pro Pro Met Pro Gly Gly Gln Leu Gln>

        1230         1240         1250         1260         1270
      *      *      *      *      *      *      *      *      *      *
    CCC CTC CAG TAT TGG CCC TTT TCT TCT GCA GAT CTC TAT AAT TGG AAA
    Pro Leu Gln Tyr Trp Pro Phe Ser Ser Ala Asp Leu Tyr Asn Trp Lys>

        1280         1290         1300         1310         1320
      *      *      *      *      *      *      *      *      *      *
    ACT AAC CAT CCC CCT TTC TCG GAG GAT CCC CAA CGC CTC ACG GGG TTG
    Thr Asn His Pro Pro Phe Ser Glu Asp Pro Gln Arg Leu Thr Gly Leu>
```

FIGURE 2, CONT.

```
              1330         1340         1350         1360
         *     *     *     *     *     *     *     *     *         (SEQ ID NO: 2) cont'd
      GTG GAG TCC CTT ATG TTC TCT CAC CAG CCT ACT TGG GAT GAT TGT CAA
      Val Glu Ser Leu Met Phe Ser His Gln Pro Thr Trp Asp Asp Cys Gln>

      1370         1380         1390         1400         1410
      *     *     *     *     *     *     *     *     *     *
      CAG CTG CTG CAG ACA CTC TTC ACA ACC GAG GAG CGA GAG AGA ATT CTG
      Gln Leu Leu Gln Thr Leu Phe Thr Thr Glu Glu Arg Glu Arg Ile Leu>

         1420         1430         1440         1450         1460
         *     *     *     *     *     *     *     *     *     *
      TTA GAG GCT AAA AAA AAT GTT CCT GGG GCC GAC GGG CGA CCC ACG CAG
      Leu Glu Ala Lys Lys Asn Val Pro Gly Ala Asp Gly Arg Pro Thr Gln>

            1470         1480         1490         1500         1510
      *     *     *     *     *     *     *     *     *     *
      TTG CAA AAT GAG ATT GAC ATG GGA TTT CCC TTG ACT CGC CCC GGT TGG
      Leu Gln Asn Glu Ile Asp Met Gly Phe Pro Leu Thr Arg Pro Gly Trp>

            1520         1530         1540         1550         1560
       *     *     *     *     *     *     *     *     *     *
      GAC TAC AAC ACG GCT GAA GGT AGG GAG AGC TTG AAA ATC TAT CGC CAG
      Asp Tyr Asn Thr Ala Glu Gly Arg Glu Ser Leu Lys Ile Tyr Arg Gln>

            1570         1580         1590         1600
         *     *     *     *     *     *     *     *
      GCT CTG GTG GCG GGT CTC CGG GGC GCC TCA AGA CGG CCC ACT AAT TTG
      Ala Leu Val Ala Gly Leu Arg Gly Ala Ser Arg Arg Pro Thr Asn Leu>

      1610      1620         1630         1640         1650
      *     *     *     *     *     *     *     *     *     *
      GCT AAG GTA AGA GAG GTG ATG CAG GGA CCG AAC GAA CCT CCC TCG GTA
      Ala Lys Val Arg Glu Val Met Gln Gly Pro Asn Glu Pro Pro Ser Val>

      1660         1670         1680         1690         1700
      *     *     *     *     *     *     *     *     *
      TTT CTT GAG AGG CTC ATG GAA GCC TTC AGG CGG TTC ACC CCT TTT GAT
      Phe Leu Glu Arg Leu Met Glu Ala Phe Arg Arg Phe Thr Pro Phe Asp>

         1710         1720         1730         1740         1750
      *     *     *     *     *     *     *     *     *     *
      CCT ACC TCA GAG GCC CAG AAA GCC TCA GTG GCC CTG GCC TTC ATT GGG
      Pro Thr Ser Glu Ala Gln Lys Ala Ser Val Ala Leu Ala Phe Ile Gly>

            1760         1770         1780         1790         1800
      *     *     *     *     *     *     *     *     *     *
      CAG TCG GCT CTG GAT ATC AGG AAG AAA CTT CAG AGA CTG GAA GGG TTA
      Gln Ser Ala Leu Asp Ile Arg Lys Lys Leu Gln Arg Leu Glu Gly Leu>

            1810         1820         1830         1840
         *     *     *     *     *     *     *     *     *
      CAG GAG GCT GAG TTA CGT GAT CTA GTG AGA GAG GCA GAG AAG GTG TAT
      Gln Glu Ala Glu Leu Arg Asp Leu Val Arg Glu Ala Glu Lys Val Tyr>

      1850      1860         1870         1880         1890
      *     *     *     *     *     *     *     *     *     *
      TAC AGA AGG GAG ACA GAA GAG GAG AAG GAA CAG AGA AAA GAA AAG GAG
      Tyr Arg Arg Glu Thr Glu Glu Glu Lys Glu Gln Arg Lys Glu Lys Glu>
```

FIGURE 2, CONT.

```
           1900          1910          1920          1930          1940              (SEQ ID NO: 2) cont'd
      *      *      *      *      *      *      *      *      *
     AGA GAA GAA AGG GAG GAA AGA CGT GAT AGA CGG CAA GAG AAG AAT TTG
     Arg Glu Glu Arg Glu Glu Arg Arg Asp Arg Arg Gln Glu Lys Asn Leu>

            1950          1960          1970          1980           1990
      *      *      *      *      *      *      *      *      *      *
     ACT AAG ATC TTG GCC GCA GTG GTT GAA GGG AAG AGC AGC AGG GAG AGA
     Thr Lys Ile Leu Ala Ala Val Val Glu Gly Lys Ser Ser Arg Glu Arg>

             2000          2010          2020          2030          2040
       *      *      *      *      *      *      *      *      *      *
     GAG AGA GAT TTT AGG AAA ATT AGG TCA GGC CCT AGA CAG TCA GGG AAC
     Glu Arg Asp Phe Arg Lys Ile Arg Ser Gly Pro Arg Gln Ser Gly Asn>

              2050          2060          2070          2080
        *      *      *      *      *      *      *      *      *
     CTG GGC AAT AGG ACC CCA CTC GAC AAG GAC CAG TGT GCG TAT TGT AAA
     Leu Gly Asn Arg Thr Pro Leu Asp Lys Asp Gln Cys Ala Tyr Cys Lys>

   2090          2100          2110          2120          2130
     *      *      *      *      *      *      *      *      *      *
     GAA AAA GGA CAC TGG GCA AGG AAC TGC CCC AAG AAG GGA AAC AAA GGA
     Glu Lys Gly His Trp Ala Arg Asn Cys Pro Lys Lys Gly Asn Lys Gly>

       2140          2150          2160          2170          2180
         *      ì      *      :      ~      *      *      *      *
     CCG AAG GTC CTA GCT CTA GAA GAA GAT AAA GAT T AGGGGAGACG
     Pro Lys Val Leu Ala Leu Glu Glu Asp Lys Asp>

             2190          2200          2210          2220          2230          2240
       *      *      *      *      *      *      *      *      *      *      *      *
    · GGGTTCGGAC CCCCTCCCCG AGCCCAGGGT AACTTTGAAG GTGGAGGGGC AACCAGTTGA

             2250          2260          2270          2280          2290          2300
       *      *      *      *      *      *      *      *      *      *      *      *
     GTTCCTGGTT GATACCGGAG CGGAGCATTC AGTGCTGCTA CAACCATTAG GAAAACTAAA

             2310          2320          2330          2340          2350
       *      *      *      *      *      *      *      *      *      *
     AGAAAAAAAA TCCTGGGTG ATG GGT GCC ACA GGG CAA CGG CAG TAT CCA TGG
                           Met Gly Ala Thr Gly Gln Arg Gln Tyr Pro Trp>

             2360          2370          2380          2390          2400
       *      *      *      *      *      *      *      *      *      *
     ACT ACC CGA AGA ACC GTT GAC TTG GGA GTG GGA CGG GTA ACC CAC TCG
     Thr Thr Arg Arg Thr Val Asp Leu Gly Val Gly Arg Val Thr His Ser>

             2410          2420          2430          2440
       *      *      *      *      *      *      *      *      *
     TTT CTG GTC ATC CCT GAG TGC CCA GTA CCC CTT CTA GGT AGA GAC TTA
     Phe Leu Val Ile Pro Glu Cys Pro Val Pro Leu Leu Gly Arg Asp Leu>

   2450          2460          2470          2480          2490
     *      *      *      *      *      *      *      *      *      *
     CTG ACC AAG ATG GGA GCT CAA ATT TCT TTT GAA CAA GGA AGA CCA GAA
     Leu Thr Lys Met Gly Ala Gln Ile Ser Phe Glu Gln Gly Arg Pro Glu>
```

FIGURE 2, CONT.

(SEQ ID NO: 2) cont'd

```
        2500         2510         2520         2530         2540
         *       *    *       *    *       *    *       *    *
GTG TCT GTG AAT AAC AAA CCC ATC ACT GTG TTG ACC CTC CAA TTA GAT
Val Ser Val Asn Asn Lys Pro Ile Thr Val Leu Thr Leu Gln Leu Asp>

           2550         2560         2570         2580         2590
         *       *    *       *    *       *    *       *    *       *
GAT GAA TAT CGA CTA TAT TCT CCC CAA GTA AAG CCT GAT CAA GAT ATA
Asp Glu Tyr Arg Leu Tyr Ser Pro Gln Val Lys Pro Asp Gln Asp Ile>

           2600         2610         2620         2630         2640
         *    *       *    *       *    *       *    *       *    *
CAG TCC TGG TTG GAG CAG TTT CCC CAA GCC TGG GCA GAA ACC GCA GGG
Gln Ser Trp Leu Glu Gln Phe Pro Gln Ala Trp Ala Glu Thr Ala Gly>

           2650         2660         2670         2680
         *    *       *    *       *    *       *    *       *
ATG GGT TTG GCA AAG CAA GTT CCC CCA CAG GTT ATT CAA CTG AAG GCC
Met Gly Leu Ala Lys Gln Val Pro Pro Gln Val Ile Gln Leu Lys Ala>

  2690         2700         2710         2720         2730
   *       *    *       *    *       *    *       *    *       *
AGT GCT ACA CCA GTA TCA GTC AGA CAG TAC CCC TTG AGT AGA GAG GCT
Ser Ala Thr Pro Val Ser Val Arg Gln Tyr Pro Leu Ser Arg Glu Ala>

  2740         2750         2760         2770         2780
         *    *       *    *       *    *       *    *       *
CGA GAA GGA ATT TGG CCG CAT GTT CAA AGA TTA ATC CAA CAG GGC ATC
Arg Glu Gly Ile Trp Pro His Val Gln Arg Leu Ile Gln Gln Gly Ile>

     2790         2800         2810         2820         2830
   *       *    *       *    *       *    *       *    *       *
CTA GTT CCT GTC CAA TCC CCT TGG AAT ACT CCC CTG CTA CCG GTT AGG
Leu Val Pro Val Gln Ser Pro Trp Asn Thr Pro Leu Leu Pro Val Arg>

        2840         2850         2860         2870         2880
   *       *    *       *    *       *    *       *    *       *
AAG CCT GGG ACC AAT GAT TAT CGA CCA GTA CAG GAC TTG AGA GAG GTC
Lys Pro Gly Thr Asn Asp Tyr Arg Pro Val Gln Asp Leu Arg Glu Val>

        2890         2900         2910         2920
         *    *       *    *       *    *       *    *
AAT AAA AGG GTG CAG GAC ATA CAC CCA ACG GTC CCG AAC CCT TAT AAC
Asn Lys Arg Val Gln Asp Ile His Pro Thr Val Pro Asn Pro Tyr Asn>

  2930         2940         2950         2960         2970
   *       *    *       *    *       *    *       *    *       *
CTC TTG AGC GCC CTC CCG CCT GAA CGG AAC TGG TAC ACA GTA TTG GAC
Leu Leu Ser Ala Leu Pro Pro Glu Arg Asn Trp Tyr Thr Val Leu Asp>

     2980         2990         3000         3010         3020
   *       *    *       *    *       *    *       *    *
TTA AAA GAT GCC TTC TTC TGC CTG AGA TTA CAC CCC ACT AGC CAA CCA
Leu Lys Asp Ala Phe Phe Cys Leu Arg Leu His Pro Thr Ser Gln Pro>

     3030         3040         3050         3060         3070
   *       *    *       *    *       *    *       *    *       *
CTT TTT ACC TTC GAA TGG AGA GAT CCA GGT ACG GGA AGA ACC GGG CAG
Leu Phe Thr Phe Glu Trp Arg Asp Pro Gly Thr Gly Arg Thr Gly Gln>
```

FIGURE 2, CONT.

(SEQ ID NO: 2) cont'd

```
        3080          3090          3100          3110          3120
    *      *      *      *      *      *      *      *      *      *
   CTC ACC TGG ACC CGA CTG CCC CAA GGG TTC AAG AAC TCC CCG ACC ATC
   Leu Thr Trp Thr Arg Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Ile>

          3130          3140          3150          3160
      *      *      *      *      *      *      *      *      *
   TTT GAC GAA GCC CTA CAC AGG GAC CTG GCC AAC TTC AGG ATC CAA CAC
   Phe Asp Glu Ala Leu His Arg Asp Leu Ala Asn Phe Arg Ile Gln His>

 3170          3180          3190          3200          3210
    *      *      *      *      *      *      *      *      *      *
   CCT CAG GTG ACC CTC CTC CAG TAC GTG GAT GAC CTG CTT CTG GCG GGA
   Pro Gln Val Thr Leu Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Gly>

    3220          3230          3240          3250          3260
       *      *      *      *      *      *      *      *      *
   GCC ACC AAA CAG GAC TGC TTA GAA GGT ACG AAG GCA CTA CTG CTG GAA
   Ala Thr Lys Gln Asp Cys Leu Glu Gly Thr Lys Ala Leu Leu Leu Glu>

       3270          3280          3290          3300          3310
    *      *      *      *      *      *      *      *      *      *
   TTG TCT GAC CTA GGC TAC AGA GCC TCT GCT AAG AAG GCC CAG ATT TGC
   Leu Ser Asp Leu Gly Tyr Arg Ala Ser Ala Lys Lys Ala Gln Ile Cys>

          3320          3330          3340          3350          3360
      *      *      *      *      *      *      *      *      *      *
   AGG AGA GAG GTA ACA TAC TTG GGG TAC AGT TTG CGG GGC GGG CAG CGA
   Arg Arg Glu Val Thr Tyr Leu Gly Tyr Ser Leu Arg Gly Gly Gln Arg>

            3370          3380          3390          3400
        *      *      *      *      *      *      *      *      *
   TGG CTG ACG GAG GCA CGG AAG AAA ACT GTA GTC CAG ATA CCG GCC CCA
   Trp Leu Thr Glu Ala Arg Lys Lys Thr Val Val Gln Ile Pro Ala Pro>

 3410          3420          3430          3440          3450
    *      *      *      *      *      *      *      *      *      *
   ACC ACA GCC AAA CAA GTG AGA GAG TTT TTG GGG ACA GCT GGA TTT TGC
   Thr Thr Ala Lys Gln Val Arg Glu Phe Leu Gly Thr Ala Gly Phe Cys>

    3460          3470          3480          3490          3500
       *      *      *      *      *      *      *      *      *
   AGA CTG TGG ATC CCG GGG TTT GCG ACC TTA GCA GCC CCA CTC TAC CCG
   Arg Leu Trp Ile Pro Gly Phe Ala Thr Leu Ala Ala Pro Leu Tyr Pro>

    3510          3520          3530          3540          3550
    *      *      *      *      *      *      *      *      *      *
   CTA ACC AAA GAA AAA GGG GGT TGC TTA CCT CAG CAG GGA GGG AAA TA AAG
   Leu Thr Lys Glu Lys Gly
                   Lys Arg Gly Leu Leu Thr Ser Ala Gly Arg Glu Ile Lys>

    3560          3570          3580          3590          3600
    *      *      *      *      *      *      *      *      *      *
   AAC AAA GAG GAA ATT CTA AGC CTA TTA GAA GCC TTA CAT TTG CCA AAA
   Asn Lys Glu Glu Ile Leu Ser Leu Leu Glu Ala Leu His Leu Pro Lys>

    3610          3620          3630          3640          3650
    *      *      *      *      *      *      *      *      *      *
   AGG CTA GCT ATT ATA CAC TGT CCT GGA CAT CAG AAA GCC AAA GAT CTC
   Arg Leu Ala Ile Ile His Cys Pro Gly His Gln Lys Ala Lys Asp Leu>
```

FIGURE 2, CONT.

(SEQ ID NO: 2) cont'd

```
          3660        3670        3680        3690
    *       *     *     *     *     *     *     *     *
   ATA TCT AGA GGG AAC CAG ATG GCT GAC CGG GTT GCC AAG CAG GCA GCC
   Ile Ser Arg Gly Asn Gln Met Ala Asp Arg Val Ala Lys Gln Ala Ala>

 3700        3710        3720        3730        3740
    *       *     *     *     *     *     *     *     *     *
   CAG GCT GTT AAC CTT CTG CCT ATA ATA GAA ACG CCC AAA GCC CCA GAA
   Gln Ala Val Asn Leu Leu Pro Ile Ile Glu Thr Pro Lys Ala Pro Glu>

       3750        3760        3770        3780        3790
          *       *     *     *     *     *     *     *     *
   CCC AGA CGA CAG TAC ACC CTA GAA GAC TGG CAA GAG ATA AAA AAG ATA
   Pro Arg Arg Gln Tyr Thr Leu Glu Asp Trp Gln Glu Ile Lys Lys Ile>

        3800        3810        3820        3830        3840
    *     *       *     *     *     *     *     *     *     *
   GAC CAG TTC TCT GAG ACT CCG GAG GGG ACC TGC TAT ACC TCA TAT GGG
   Asp Gln Phe Ser Glu Thr Pro Glu Gly Thr Cys Tyr Thr Ser Tyr Gly>

          3850        3860        3870        3880        3890
       *       *     *     *     *     *     *     *     *     *
   AAG GAA ATC CTG CCC CAC AAA GAA GGG TTA GAA TAT GTC CAA CAG ATA
   Lys Glu Ile Leu Pro His Lys Glu Gly Leu Glu Tyr Val Gln Gln Ile>

             3900        3910        3920        3930
          *       *     *     *     *     *     *     *
   CAT CGT CTA ACC CAC CTA GGA ACT AAA CAC CTG CAG CAG TTG GTC AGA
   His Arg Leu Thr His Leu Gly Thr Lys His Leu Gln Gln Leu Val Arg>

 3940        3950        3960        3970        3980
    *       *     *     *     *     *     *     *     *     *
   ACA TCC CCT TAT CAT GTT CTG AGG CTA CCA GGA GTG GCT GAC TCG GTG
   Thr Ser Pro Tyr His Val Leu Arg Leu Pro Gly Val Ala Asp Ser Val>

    3990        4000        4010        4020        4030
       *       *     *     *     *     *     *     *     *
   GTC AAA CAT TGT GTG CCC TGC CAG CTG GTT AAT GCT AAT CCT TCC AGA
   Val Lys His Cys Val Pro Cys Gln Leu Val Asn Ala Asn Pro Ser Arg>

      4040        4050        4060        4070        4080
    *     *     *     *     *     *     *     *     *     *
   ATA CCT CCA GGA AAG AGA CTA AGG GGA AGC CAC CCA GGC GCT CAC TGG
   Ile Pro Pro Gly Lys Arg Leu Arg Gly Ser His Pro Gly Ala His Trp>

       4090        4100        4110        4120        4130
    *       *     *     *     *     *     *     *     *     *
   GAA GTG GAC TTC ACT GAG GTA AAG CCG GCT AAA TAC GGA AAC AAA TAT
   Glu Val Asp Phe Thr Glu Val Lys Pro Ala Lys Tyr Gly Asn Lys Tyr>

          4140        4150        4160        4170
       *       *     *     *     *     *     *     *     *
   CTA TTG GTT TTT GTA GAC ACC TTT TCA GGA TGG GTA GAG GCT TAT CCT
   Leu Leu Val Phe Val Asp Thr Phe Ser Gly Trp Val Glu Ala Tyr Pro>

 4180        4190        4200        4210        4220
    *       *     *     *     *     *     *     *     *     *
   ACT AAA AAA GAG ACT TCA ACC GTG GTG GCT AAG AAA ATA CTG GAG GAA
   Thr Lys Lys Glu Thr Ser Thr Val Val Ala Lys Lys Ile Leu Glu Glu>
```

FIGURE 2, CONT.

```
      4230        4240         4250        4260        4270       (SEQ ID NO: 2) cont'd
       *     *     *     *     *     *    ·  *     *     *
     ATT TTT CCA AGA TTT GGA ATA CCT AAG GTA ATA GGG TCA GAC AAT GGT
     Ile Phe Pro Arg Phe Gly Ile Pro Lys Val Ile Gly Ser Asp Asn Gly>

        4280        4290         4300        4310         4320
     *     *     *     *     *     *     *     *      *      *
     CCA GCT TTC GTT GCC CAG GTA AGT CAG GGA CTG GCC AAG ATA TTG GGG
     Pro Ala Phe Val Ala Gln Val Ser Gln Gly Leu Ala Lys Ile Leu Gly>

          4330        4340        4350        4360       4370        4380
       *     *     *     *     *     *     *     *     *     *      *     *
     ATT GAT TG A AAA CTG CAT TGT GCA TAC AGA CCC CAA AGC TCA GGA CAG
     Ile Asp       Lys Leu His Cys Ala Tyr Arg Pro Gln Ser Ser Gly Gln>

            4380         4390        4400        4410
         *     *     *     *     *     *     *     *     *
     GTA GAG AGG ATG AAT AGA ACC ATT AAA GAG ACC CTT ACC AAA TTG ACC
     Val Glu Arg Met Asn Arg Thr Ile Lys Glu Thr Leu Thr Lys Leu Thr>

    4420        4430         4440        4450        4460
     *     *     *     *     *     *     *     *     *     *
     ACA GAG ACT GGC ATT AAT GAT TGG ATG GCT CTC CTG CCC TTT GTG CTT
     Thr Glu Thr Gly Ile Asn Asp Trp Met Ala Leu Leu Pro Phe Val Leu>

       4470        4480         4490        4500        4510
        *     *     *     :     *     *·     *     *     *
     TTT AGG GTG AGG AAC ACC CCT GGA CAG TTT GGG CTG ACC CCC TAT AAA
     Phe Arg Val Arg Asn Thr Pro Gly Gln Phe Gly Leu Thr Pro Tyr Lys>

        4520        4530         4540        4550        4560
     *     *     *     *     *     *     *     *     *     *
     TTG CTC TAC GGG GGA CCC CCC CCG TTG GCA GAA ATT GCC TTT GCA CAT
     Leu Leu Tyr Gly Gly Pro Pro Pro Leu Ala Glu Ile Ala Phe Ala His>

          4570        4580        4590        4600        4610
       *     *     *     *     *     *     *     *     *     *
     AGT GCT GAT GTG CTG CTT TCC CAG CCT TTG TTC TCT AGG CTC AAG GCG
     Ser Ala Asp Val Leu Leu Ser Gln Pro Leu Phe Ser Arg Leu Lys Ala>

           4620        4630        4640       · 4650
        *     *     *     *     *     * ·    *     *
     CTC GAG TGG GTG AGG CAG CGA GCG TGG AAG CAG CTC CGG GAG GCC TAC
     Leu Glu Trp Val Arg Gln Arg Ala Trp Lys Gln Leu Arg Glu Ala Tyr>

    4660        4670         4680        4690        4700
     *     *     *     *     *     *     *     *     *     *
     TCA GGA GGA GAC TTG CAA GTT CCA CAT CGC TTC CAA GTT GGA GAT TCA
     Ser Gly Gly Asp Leu Gln Val Pro His Arg Phe Gln Val Gly Asp Ser>

       4710        4720       · 4730        4740        4750
        *     *     *     *     *     *     *     *     *·
     GTC TAT GTT AGA CGC CAC CGT GCA GGA AAC CTC GAG ACT CGG TAG AAG
     Val Tyr Val Arg Arg His Arg Ala Gly Asn Leu Glu Thr Arg *** Lys>

        4760        4770       · 4780        4790        4800
     *     *     *     *     *     *     *     *     *     *
     GGA CCT TAT CTC GTA CTT TTG ACC ACA CCA ACG GCT GTG AAA GTC GAA
     Gly Pro Tyr Leu Val Leu Leu Thr Thr Pro Thr Ala Val Lys Val Glu>
```

FIGURE 2, CONT.

```
           4810        4820        4830        4840        4850   (SEQ ID NO: 2) cont'd
    *       *      *     *        *      *      *      *      *      *
   GGA ATC CCC TTA AGC TTC GCC TCC ATC GCG TGG TTC CTT ACT CTG TCA
   Gly Ile Pro Leu Ser Phe Ala Ser Ile Ala Trp Phe Leu Thr Leu Ser>

             4860        4870        4880        4890
      *       *     *      *      *      *      *     *      *
   ATA ACT CCT CAA GTT AAT GGT AAA CGC CTT GTG GAC AGC CCG AAC TCC
   Ile Thr Pro Gln Val Asn Gly Lys Arg Leu Val Asp Ser Pro Asn Ser>

  4900        4910        4920        4930        4940
   *       *     *      *       *     *      *      *     *       *
   CAT AAA CCC TTA TCT CTC ACC TGG TTA CTT ACT GAC TCC GGT ACA GGT
   His Lys Pro Leu Ser Leu Thr Trp Leu Leu Thr Asp Ser Gly Thr Gly>

    4950        4960        4970        4980        4990
     *      *      *      *      *      *      *      *      *
   ATT AAT ATT AAC AGC ACT CAA GGG GAG GCT CCC TTG GGG ACC TGG TGG
   Ile Asn Ile Asn Ser Thr Gln Gly Glu Ala Pro Leu Gly Thr Trp Trp>

       5000        5010        5020        5030        5040
   *       *      *      *      *      *      *      *      *       *
   CCT GAA TTA TAT GTC TGC CTT CGA TCA GTA ATC CCT GGT CTC AAT GAC
   Pro Glu Leu Tyr Val Cys Leu Arg Ser Val Ile Pro Gly Leu Asn Asp>

        5050        5060        5070        5080        5090
     *      *      *      *      *      *      *      *      *      *
   CAG GCC ACA CCC CCC GAT GTA CTC CGT GCT TAC GGG TTT TAC GTT TGC
   Gln Ala Thr Pro Pro Asp Val Leu Arg Ala Tyr Gly Phe Tyr Val Cys>

           5100        5110        5120        5130
        *       *     *      *      *      *      *      *     *
   CCA GGA CCC CCA AAT AAT GAA GAA TAT TGT GGA AAT CCT CAG GAT TTC
   Pro Gly Pro Pro Asn Asn Glu Glu Tyr Cys Gly Asn Pro Gln Asp Phe>

  5140        5150        5160        5170        5180
   *       *     *      *      *      *      *      *     *       *
   TTT TGC AAG CAA TGG AGC TGC ATA ACT TCT AAT GAT GGG AAT TGG AAA
   Phe Cys Lys Gln Trp Ser Cys Ile Thr Ser Asn Asp Gly Asn Trp Lys>

     5190        5200        5210        5220        5230
      *       *      *      *      *      *      *      *      *
   TGG CCA GTC TCT CAG CAA GAC AGA GTA AGT TAC TCT TTT GTT AAC AAT
   Trp Pro Val Ser Gln Gln Asp Arg Val Ser Tyr Ser Phe Val Asn Asn>

     5240        5250        5260        5270        5280
   *       *      *      *      *       *      *      *      *      *
   CCT ACC AGT TAT AAT CAA TTT AAT TAT GGC CAT GGG AGA TGG AAA GAT
   Pro Thr Ser Tyr Asn Gln Phe Asn Tyr Gly His Gly Arg Trp Lys Asp>

        5290        5300        5310        5320        5330
      *       *      *      *      *      *      *      *     *      *
   TGG CAA CAG CGG GTA CAA AAA GAT GTA CGA AAT AAG CAA ATA AGC TGT
   Trp Gln Gln Arg Val Gln Lys Asp Val Arg Asn Lys Gln Ile Ser Cys>

           5340        5350        5360        5370
        *      *      *      *      *      *      *      *     *
   CAT TCG TTA GAC CTA GAT TAC TTA AAA ATA AGT TTC ACT GAA AAA GGA
   His Ser Leu Asp Leu Asp Tyr Leu Lys Ile Ser Phe Thr Glu Lys Gly>
```

FIGURE 2, CONT.

(SEQ ID NO: 2) cont'd

```
       5380          5390          5400          5410          5420
        *        *    *        *    *        *    *        *    *        *
      AAA CAA GAA AAT ATT CAA AAG TGG GTA AAT GGT ATA TCT TGG GGA ATA
      Lys Gln Glu Asn Ile Gln Lys Trp Val Asn Gly Ile Ser Trp Gly Ile>

          5430          5440          5450          5460          5470
           *        *    *        *    *        *    *        *    *
         GTG TAC TAT GGA GGC TCT GGG AGA AAG AAA GGA TCT GTT CTG ACT ATT
         Val Tyr Tyr Gly Gly Ser Gly Arg Lys Lys Gly Ser Val Leu Thr Ile>

            5480          5490          5500          5510          5520
         *    *        *    *        *    *        *    *        *    *
        CGC CTC AGA ATA GAA ACT CAG ATG GAA CCT CCG GTT GCT ATA GGA CCA
        Arg Leu Arg Ile Glu Thr Gln Met Glu Pro Pro Val Ala Ile Gly Pro>

                 5530          5540          5550          5560
              *        *    *        *    *        *    *        *    *
            AAT AAG GGT TTG GCC GAA CAA GGA CCT CCA ATC CAA GAA CAG
            Asn Lys Gly Leu Ala Glu Gln Gly Pro Pro Ile Gln Glu Gln>

         5570          5580          5590          5600          5610
        *    *        *    *        *    *        *    *        *    *
      AGG CCA TCT CCT AAC CCC TCT GAT TAC AAT ACA ACC TCT GGA TCA GTC
      Arg Pro Ser Pro Asn Pro Ser Asp Tyr Asn Thr Thr Ser Gly Ser Val>

           5620          5630          5640          5650          5660
          *        *    *        *    *        *    *        *
        CCC ACT GAG CCT AAC ATC ACT ATT AAA ACA GGG GCG AAA CTT TTT AGC
        Pro Thr Glu Pro Asn Ile Thr Ile Lys Thr Gly Ala Lys Leu Phe Ser>

              5670          5680          5690          5700
           *        *    *        *    *        *    *        *    *
         CTC ATC CAG GGA GCT TTT CAA GCT CTT AAC TCC ACG ACT CCA GAG GCT
         Leu Ile Gln Gly Ala Phe Gln Ala Leu Asn Ser Thr Thr Pro Glu Ala>

      5710          5720          5730          5740          5750
        *        *    *        *    *        *    *        *    *        *
      ACC TCT TCT TGT TGG CTT TGC TTA GCT TCG GGC CCA CCT TAC TAT GAG
      Thr Ser Ser Cys Trp Leu Cys Leu Ala Ser Gly Pro Pro Tyr Tyr Glu>

         5760          5770          5780          5790          5800
          *        *    *        *    *        *    *        *    *
        GGA ATG GCT AGA GGA GGG AAA TTC AAT GTG ACA AAG GAA CAT AGA GAC
        Gly Met Ala Arg Gly Gly Lys Phe Asn Val Thr Lys Glu His Arg Asp>

         5810          5820          5830          5840          5850
        *    *        *    *        *    *        *    *        *    *
      CAA TGT ACA TGG GGA TCC CAA AAT AAG CTT ACC CTT ACT GAG GTT TCT
      Gln Cys Thr Trp Gly Ser Gln Asn Lys Leu Thr Leu Thr Glu Val Ser>

            5860          5870          5880          5890          5900
           *        *    *        *    *        *    *        *    *    *
         GGA AAA GGC ACC TGC ATA GGG ATG GTT CCC CCA TCC CAC CAA CAC CTT
         Gly Lys Gly Thr Cys Ile Gly Met Val Pro Pro Ser His Gln His Leu>

              5910          5920          5930          5940
           *        *    *        *    *        *    *        *    *
         TGT AAC CAC ACT GAA GCC TTT AAT CGA ACC TCT GAG AGT CAA TAT CTG
         Cys Asn His Thr Glu Ala Phe Asn Arg Thr Ser Glu Ser Gln Tyr Leu>
```

FIGURE 2, CONT.

5950   5960   5970   5980   5990   (SEQ ID NO: 2) cont'd

```
GTA CCT GGT TAT GAC AGG TGG TGG GCA TGT AAT ACT GGA TTA ACC CCT
Val Pro Gly Tyr Asp Arg Trp Trp Ala Cys Asn Thr Gly Leu Thr Pro>
```

6000   6010   6020   6030   6040

```
TGT GTT TCC ACC TTG GTT TTC AAC CAA ACT AAA GAC TTT TGC GTT ATG
Cys Val Ser Thr Leu Val Phe Asn Gln Thr Lys Asp Phe Cys Val Met>
```

6050   6060   6070   6080   6090

```
GTC CAA ATT GTC CCC CGG GTG TAC TAC TAT CCC GAA AAA GCA GTC CTT
Val Gln Ile Val Pro Arg Val Tyr Tyr Tyr Pro Glu Lys Ala Val Leu>
```

6100   6110   6120   6130   6140

```
GAT GAA TAT GAC TAT AGA TAT AAT CGG CCA AAA AGA GAG CCC ATA TCC
Asp Glu Tyr Asp Tyr Arg Tyr Asn Arg Pro Lys Arg Glu Pro Ile Ser>
```

6150   6160   6170   6180

```
CTG ACA CTA GCT GTA ATG CTC GGA TTG GGA GTG GCT GCA GGC GTG GGA
Leu Thr Leu Ala Val Met Leu Gly Leu Gly Val Ala Ala Gly Val Gly>
```

6190   6200   6210   6220   6230

```
ACA GGA ACG GCT GCC CTA ATC ACA GGA CCG CAA CAG CTG GAG AAA GGA
Thr Gly Thr Ala Ala Leu Ile Thr Gly Pro Gln Gln Leu Glu Lys Gly>
```

6240   6250   6260   6270   6280

```
CTT AGT AAC CTA CAT CGA ATT GTA ACG GAA GAT CTC CAA GCC CTA GAA
Leu Ser Asn Leu His Arg Ile Val Thr Glu Asp Leu Gln Ala Leu Glu>
```

6290   6300   6310   6320   6330

```
AAA TCT GTC AGT AAC CTG GAG GAA TCC CTA ACC TCC TTA TCT GAA GTG
Lys Ser Val Ser Asn Leu Glu Glu Ser Leu Thr Ser Leu Ser Glu Val>
```

6340   6350   6360   6370   6380

```
GTT CTA CAG AAC AGA AGG GGG TTA GAT CTG TTA TTT CTA AAA GAA GGA
Val Leu Gln Asn Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys Glu Gly>
```

6390   6400   6410   6420

```
GGG TTA TGT GTA GCC TTA AAA GAG GAA TGC TGC TTC TAT GTA GAT CAC
Gly Leu Cys Val Ala Leu Lys Glu Glu Cys Cys Phe Tyr Val Asp His>
```

6430   6440   6450   6460   6470

```
TCA GGA GCC ATC AGA GAC TCC ATG AGC AAG CTT AGA GAA AGG TTA GAG
Ser Gly Ala Ile Arg Asp Ser Met Ser Lys Leu Arg Glu Arg Leu Glu>
```

6480   6490   6500   6510   6520

```
AGG CGT CGA AGG GAA AGA GAG GCT GAC CAG GGG TGG TTT GAA GGA TGG
Arg Arg Arg Arg Glu Arg Glu Ala Asp Gln Gly Trp Phe Glu Gly Trp>
```

FIGURE 2, CONT.

```
             6530           6540           6550           6560           6570      (SEQ ID NO: 2) cont'd
        *      *      *      *      *      *      *      *      *      *
     TTC AAC AGG TCT CCT TGG ATG ACC ACC CTG CTT TCT GCT CTG ACG GGG
     Phe Asn Arg Ser Pro Trp Met Thr Thr Leu Leu Ser Ala Leu Thr Gly>

              6580           6590           6600           6610           6620
         *      *      *      *      *      *      *      *      *      *
     CCC CTA GTA GTC CTG CTC CTG TTA CTT ACA GTT GGG CCT TGC TTA ATT
     Pro Leu Val Val Leu Leu Leu Leu Leu Thr Val Gly Pro Cys Leu Ile>

               6630           6640           6650           6660
          *      *      *      *      *      *      *      *      *
     AAT AGG TTT GTT GCC TTT GTT AGA GAA CGA GTG AGT GCA GTC CAG ATC
     Asn Arg Phe Val Ala Phe Val Arg Glu Arg Val Ser Ala Val Gln Ile>

   6670        6680           6690           6700           6710
      *      *      *      *      *      *      *      *      *      *
     ATG GTA CTT AGG CAA CAG TAC CAA GGC CTT CTG AGC CAA GGA GAA ACT
     Met Val Leu Arg Gln Gln Tyr Gln Gly Leu Leu Ser Gln Gly Glu Thr>

        6720      6730        6740        6750        6760        6770
          *      *      *      *      *      *      *      *      *      *
     GAC CTC TAGCCTTC CCAGTTCTAA GATTAGAACT ATTAACAAGA CAAGAAGTGG
     Asp Leu>

             6780           6790           6800           6810           6820           6830
        *      *      *      *      *      *      *      *      *      *      *      *
     GGAATGAAAG GATGAAAATG CAACCTAACC CTCCCAGAAC CCAGGAAGTT AATAAAAAGC

             6840           6850           6860           6870           6880           6890
        *      *      *      *      *      *      *      *      *      *      *      *
     TCTAAATGCC CCCGAATTCC AGACCCTGCT GGCTGCCAGT AAATAGGTAG AAGGTCACAC

             6900           6910           6920           6930           6940           6950
        *      *      *      *      *      *      *      *      *      *      *      *
     TTCCTATTGT TCCAGGGCCT GCTATCCTGG CCTAAGTAAG ATAACAGGAA ATGAGTTGAC

             6960           6970           6980           6990           7000           7010
        *      *      *      *      *      *      *      *      *      *      *      *
     TAATCGCTTA TCTGGATTCT GTAAAACTGA CTGGCACCAT AGAAGAATTG ATTACACATT

             7020           7030           7040           7050           7060           7070
        *      *      *      *      *      *      *      *      *      *      *      *
     GACAGCCCTA GTGACCTATC TCAACTGCAA TCTGTCACTC TGCCCAGGAG CCCACGCAGA

             7080           7090           7100           7110           7120           7130
        *      *      *      *      *      *      *      *      *      *      *      *
     TGCGGACCTC CGGAGCTATT TTAAAATGAT TGGTCCACGG AGCGCGGGCT CTCGATATTT

             7140           7150           7160           7170           7180           7190
        *      *      *      *      *      *      *      *      *      *      *      *
     TAAAATGATT GGTCCATGGA GCGCGGGCTC TCGATATTTT AAAATGATTG GTTTGTGACG

             7200           7210           7220           7230           7240           7250
        *      *      *      *      *      *      *      *      *      *      *      *
     CACAGGCTTT GTTGTGAACC CCATAAAAGC TGTCCCGATT CCGCACTCGG GGCCGCAGTC
```

FIGURE 2, CONT.

```
       7260        7270        7280        7290        7300        7310      (SEQ ID NO: 2) cont'd
       *     *     *     *     *     *     *     *     *     *     *     `
    CTCTACCCCT GCGTGGTGTA CGACTGTGGG CCCCAGCGCG CTTGGAATAA AAATCCTCTT


       7320        7330
       *     *     *     *
    GCTGTTTGCA TCAAAAAAAA AAA
```

FIGURE 2, CONT.

```
        10          20          30          40          50          60      (SEQ ID NO: 3)
     *     *     *     *     *     *     *     *     *     *     *     *
  GCGTGGTGTA CGACTGTGGG CCCCAGCGCG CTTGGAATAA AAATCCTCTT GCTGTTTGCA

        70          80          90         100         110         120
     *     *     *     *     *     *     *     *     *     *     *     *
  TCAAGACCGC TTCTCGTGAG TGATTAAGGG GAGTCGCCTT TTCCGAGCCT GGAGGTTCTT

       130         140         150         160         170         180
     *     *     *     *     *     *     *     *     *     *     *     *
  TTTGCTGGTC TTACATTTGG GGGCTCGTCC GGGATCTGTC GCGGCCACCC CTAACACCCG

       190         200         210         220         230         240
     *     *     *     *     *     *     *     *     *     *     *     *
  AGAACCGACT TGGAGGTAAA AAGGATCCTC TTTTTAACGT GTATGCATGT ACCGGCCGGC

       250         260         270         280         290         300
     *     *     *     *     *     *     *     *     *     *     *     *
  GTCTCTGTTC TGAGTGTCTG TTTTCAGTGG TGCGCGCTTT CGGTTTGCAG CTGTCCTCTC

       310         320         330         340         350         360
     *     *     *     *     *     *     *     *     *     *     *     *
  AGGCCGTAAG GGCTGGGGGA CTGTGATCAG CAGACGTGCT AGGAGGATCA CAGGCTGCTG

       370         380         390         400         410         420
     *     *     *     *     *     *     *     *     *     *     *     *
  CCCTGGGGGA CGCCCCGGGA GGTGAGGAGA GCCAGGGACG CCTGGTGGTC TCCTACTGTC

       430         440         450         460         470         480
     *     *     *     *     *     *     *     *     *     *     *     *
  GGTCAGAGGA CCGAATTCTG TTGCTGAAGC GAAAGCTTCC CCCTCCGCGA CCGTCCGACT

       490         500         510         520         530         540
     *     *     *     *     *     *     *     *     *     *     *     *
  CTTTTGCCTG CTTGTGGAAG ACGTGGACGG GTCACGTGTG TCTGGATCTG TTGGTTTCTG

       550         560         570         580         590
     *     *     *     *     *     *     *     *     *     *     *
  TTTTGTGTGT CTTTGTCTTG TGTGTCCTTG TCTACAGTTT TAAT ATG GGA CAG ACG
                                                   Met Gly Gln Thr>

     600         610         620         630         640
     *     *     *     *     *     *     *     *     *
  GTG ACG ACC CCT CTT AGT TTG ACT CTC GAC CAT TGG ACT GAA GTT AAA
  Val Thr Thr Pro Leu Ser Leu Thr Leu Asp His Trp Thr Glu Val Lys>

        650         660         670         680         690
   *     *     *     *     *     *     *     *     *     *     *
  TCC AGG GCT CAT AAT TTG TCA GTT CAG GTT AAG AAG GGA CCT TGG CAG
  Ser Arg Ala His Asn Leu Ser Val Gln Val Lys Lys Gly Pro Trp Gln>

        700         710         720         730         740
   *     *     *     *     *     *     *     *     *     *     *
  ACT TTC TGT GTC TCT GAA TGG CCG ACA TTC GAT GTT GGA TGG CCA TCA
  Thr Phe Cys Val Ser Glu Trp Pro Thr Phe Asp Val Gly Trp Pro Ser>
```

FIGURE 3

(SEQ ID NO: 3) cont'd

```
         750        760        770        780
     *    *    *    *    *    *    *    *    *
GAG GGG ACC TTT AAT TCT GAG ATT ATC CTG GCT GTT AAA GCA GTT ATT
Glu Gly Thr Phe Asn Ser Glu Ile Ile Leu Ala Val Lys Ala Val Ile>

  790        800        810        820        830
     *    *    *    *    *    *    *    *    *
TTT CAG ACT GGA CCC GGC TCT CAT CCC GAT CAG GAG CCC TAT ATC CTT
Phe Gln Thr Gly Pro Gly Ser His Pro Asp Gln Glu Pro Tyr Ile Leu>

     840        850        860        870        880
     *    *    *    *    *    *    *    *    *
ACG TGG CAA GAT TTG GCA GAG GAT CCT CCG CCA TGG GTT AAA CCA TGG
Thr Trp Gln Asp Leu Ala Glu Asp Pro Pro Pro Trp Val Lys Pro Trp>

        890        900        910        920        930
  *    *    *    *    · *    *    *  *    *    *    *
CTG AAT AAG CCA AGA AAG CCA GGT CCC CGA ATT CTG GCT CTT GGA GAG
Leu Asn Lys Pro Arg Lys Pro Gly Pro Arg Ile Leu Ala Leu Gly Glu>

        940        950        960        970        980
     *    *    *    *    *    *    *    *    *    *
AAA AAC AAA CAC TCG GCT GAA AAA GTC AAG CCC TCT CCT CAT ATC TAC
Lys Asn Lys His Ser Ala Glu Lys Val Lys Pro Ser Pro His Ile Tyr>

        990        1000       1010       1020
     *    *    *    *    *    *    *    *    *
CCC GAG ATT GAG GAG CCA CCG GCT TGG CCG GAA CCC CAA TCT GTT CCC
Pro Glu Ile Glu Glu Pro Pro Ala Trp Pro Glu Pro Gln Ser Val Pro>

1030       1040       1050       1060       1070
  *    *    *    *    *    *    *    *    *    *
CCA CCC CCT TAT CTG GCA CAG GGT GCC GCG AGG GGA CCC TTT GCC CCT
Pro Pro Pro Tyr Leu Ala Gln Gly Ala Ala Arg Gly Pro Phe Ala Pro>

  1080       1090       1100       1110       1120
     *    *    *    *    *    *    *    *    *
CCT GGA GCT CCG GCG GTG GAG GGA CCT GCT GCA GGG ACT CGG AGC CGG
Pro Gly Ala Pro Ala Val Glu Gly Pro Ala Ala Gly Thr Arg Ser Arg>

   1130       1140       1150       1160       1170
  *    *    *    *    *    *    *    *    *    *
AGG GGC GCC ACC CCG GAG CGG ACA GAC GAG ATC GCG ACA TTA CCG CTG
Arg Gly Ala Thr Pro Glu Arg Thr Asp Glu Ile Ala Thr Leu Pro Leu>

     1180       1190       1200       1210       1220
  *    *    *    *    *    *    *    *    *    *
CGC ACG TAC GGC CCT CCC ACA CCG GGG GGC CAA TTG CAG CCC CTC CAG
Arg Thr Tyr Gly Pro Pro Thr Pro Gly Gly Gln Leu Gln Pro Leu Gln>

     1230       1240       1250       1260
     *    *    *    *    *    *    *    *    *
TAT TGG CCC TTT TCT TCT GCA GAT CTC TAT AAT TGG AAA ACT AAC CAT
Tyr Trp Pro Phe Ser Ser Ala Asp Leu Tyr Asn Trp Lys Thr Asn His>

1270       1280       1290       1300       1310
  *    *    *    *    *    *    *    *    *    *
CCC CCT TTC TCG GAG GAT CCC CAA CGC CTC ACG GGG TTG GTG GAG TCC
Pro Pro Phe Ser Glu Asp Pro Gln Arg Leu Thr Gly Leu Val Glu Ser>
```

FIGURE 3, CONT.

(SEQ ID NO: 3) cont'd

```
        1320          1330          1340          1350          1360
         *      *      *        *      *       *       *      *       *
        CTT ATG TTC TCT CAC CAG CCT ACT TGG GAT GAT TGT CAA CAG CTG CTG
        Leu Met Phe Ser His Gln Pro Thr Trp Asp Asp Cys Gln Gln Leu Leu>

          1370          1380          1390          1400          1410
         *      *      *      *      *      *      *      *      *      *
        CAG ACA CTC TTC ACA ACC GAG GAG CGA GAG AGA ATT CTA TTA GAG GCT
        Gln Thr Leu Phe Thr Thr Glu Glu Arg Glu Arg Ile Leu Leu Glu Ala>

          1420          1430          1440          1450          1460
        *.      *      *      *      *      *      *      *      *      *
        AGA AAA AAT GTT CCT GGG GCC GAC GGG CGA CCC ACG CGG TTG CAA AAT
        Arg Lys Asn Val Pro Gly Ala Asp Gly Arg Pro Thr Arg Leu Gln Asn>

               1470          1480          1490          1500
         *      *      *      *      *      *      *      *      *      *
        GAG ATT GAC ATG GGA TTT CCC TTA ACT CGC CCC GGT TGG GAC TAC AAC
        Glu Ile Asp Met Gly Phe Pro Leu Thr Arg Pro Gly Trp Asp Tyr Asn>

       1510          1520          1530          1540          1550
         *      *      *      *      *      *      *      *      *      *
        ACG GCT GAA GGT AGG GAG AGC TTG AAA ATC TAT CGC CAG GCT CTG GTG
        Thr Ala Glu Gly Arg Glu Ser Leu Lys Ile Tyr Arg Gln Ala Leu Val>

          1560          1570          1580          1590          1600
         *      *      *      *      *      *      *      *      *      *
        GCG GGT CTC CGG GGC GCC TCA AGA CGG CCC ACT AAT TTG GCT AAG GTA
        Ala Gly Leu Arg Gly Ala Ser Arg Arg Pro Thr Asn Leu Ala Lys Val>

          1610          1620          1630          1640          1650
         *      *      *      *      *      *      *      *      *      *
        AGA GAA GTG ATG CAG GGA CCG AAT GAA CCC CCC TCT GTT TTT CTT GAG
        Arg Glu Val Met Gln Gly Pro Asn Glu Pro Pro Ser Val Phe Leu Glu>

          1660          1670          1680          1690          1700
         *      *      *      *      *      *      *      *      *      *
        AGG CTC TTG GAA GCC TTC AGG CGG TAC ACC CCT TTT GAT CCC ACC TCA
        Arg Leu Leu Glu Ala Phe Arg Arg Tyr Thr Pro Phe Asp Pro Thr Ser>

               1710          1720          1730          1740
         *      *      *      *      *      *      *      *      *      *
        GAG GCC CAA AAA GCC TCA GTG GCT TTG GCC TTT ATA GGA CAG TCA GCC
        Glu Ala Gln Lys Ala Ser Val Ala Leu Ala Phe Ile Gly Gln Ser Ala>

       1750          1760          1770          1780          1790
         *      *      *      *      *      *      *      *      *      *
        TTG GAT ATT AGA AAG AAG CTT CAG AGA CTG GAA GGG TTA CAG GAG GCT
        Leu Asp Ile Arg Lys Lys Leu Gln Arg Leu Glu Gly Leu Gln Glu Ala>

          1800          1810          1820          1830          1840
         *      *      *      *      *      *      *      *      *      *
        GAG TTA CGT GAT CTA GTG AAG GAG GCA GAG AAA GTA TAT TAC AAA AGG
        Glu Leu Arg Asp Leu Val Lys Glu Ala Glu Lys Val Tyr Tyr Lys Arg>

          1850          1860          1870          1880          1890
         *      *      *      *      *      *      *      *      *      *
        GAG ACA GAA GAA GAA AGG GAA CAA AGA AAA GAG AGA GAA AGA GAG GAA
        Glu Thr Glu Glu Glu Arg Glu Gln Arg Lys Glu Arg Glu Arg Glu Glu>
```

FIGURE 3, CONT.

(SEQ ID NO: 3) cont'd

```
        1900        1910        1920        1930        1940
     *      *     *     *    *      *     *      *     *      *
   AGG GAG GAA AGA CGT AAT AAA CGG CAA GAG AAG AAT TTG ACT AAG ATC
   Arg Glu Glu Arg Arg Asn Lys Arg Gln Glu Lys Asn Leu Thr Lys Ile>


            1950        1960        1970        1980
       *      *     *      *     *      *     *      *     *
   TTG GCT GCA GTG GTT GAA GGG AAA AGC AAT ACG GAA AGA GAG AGA GAT
   Leu Ala Ala Val Val Glu Gly Lys Ser Asn Thr Glu Arg Glu Arg Asp>

                          •
  1990        2000        2010        2020        2030
     *      *      *      *     *      *     *      *     *      *
   TTT AGG AAA ATT AGG TCA GGC CCT AGA CAG TCA GGG AAC CTG GGC AAT
   Phe Arg Lys Ile Arg Ser Gly Pro Arg Gln Ser Gly Asn Leu Gly Asn>


     2040        2050        2060        2070        2080
      *      *      *     *.     *      *    .     *     *      *
   AGG ACC CCA CTC GAC AAG GAC CAA TGT GCA TAT TGT AAA GAA AGA GGA
   Arg Thr Pro Leu Asp Lys Asp Gln Cys Ala Tyr Cys Lys Glu Arg Gly>


        2090        2100        2110        2120        2130
     *      *     *      *     *      *     *      *     *      *
   CAC TGG GCA AGG AAC TGC CCC AAG AAG GGA AAC AAA GGA CCA AGG ATC
   His Trp Ala Arg Asn Cys Pro Lys Lys Gly Asn Lys Gly Pro Arg Ile>.


        2140        2150        2160        2170        2180
      *      *     *      *     *      *     *      *     *      *
   CTA GCT CTA GAA GAA GAT AAA GAT TAGG GGAGACGGGG TTCGGACCCC
   Leu Ala Leu Glu Glu Asp Lys Asp>


        2190        2200        2210        2220        2230        2240
       *      *     *      *     *      *     *      *     *      *     *      *
   CTCCCCGAGC CCAGGGTAAC TTTGAAGGTG GAGGGGCAAC CAGTTGAGTT CCTGGTTGAT


        2250        2260        2270        2280        2290        2300
      *      *     *      *    .*      *     *      *     *      *     *      *
   ACCGGAGCGA AACATTCAGT GCTACTACAG CCATTAGGAA AACTAAAAGA TAAAAAATCC


           2310        2320        2330        2340        2350
         *      *     *      *     *      *     *      *     *      *
   TGGGTG ATG GGT GCC ACA GGG CAA CAA CAG TAT CCA TGG ACT ACC CGA AGA
          Met Gly Ala Thr Gly Gln Gln Gln Tyr Pro Trp Thr Thr Arg Arg>


        2360        2370        2380        2390
      *      *     *      *     *      *     *      *     *
   ACA GTT GAC TTG GGA GTG GGA CGG GTA ACC CAC TCG TTT CTG GTC ATA
   Thr Val Asp Leu Gly Val Gly Arg Val Thr His Ser Phe Leu Val Ile>


  2400        2410        2420        2430        2440
     *      *     *      *     *      *     *      *     *      *
   CCT GAG TGC CCA GCA CCC CTC TTA GGT AGA GAC TTA TTG ACC AAG ATG
   Pro Glu Cys Pro Ala Pro Leu Leu Gly Arg Asp Leu Leu Thr Lys Met>


  2450        2460        2470        2480        2490
     *      *     *      *     *      *     *      *     *      *
   GGA GCA CAA ATT TCT TTT GAA CAA GGG AAA CCA GAA GTG TCT GCA AAT
   Gly Ala Gln Ile Ser Phe Glu Gln Gly Lys Pro Glu Val Ser Ala Asn>
```

FIGURE 3, CONT.

```
      2500          2510          2520          2530          2540             (SEQ ID NO: 3) cont'd
       *        *     *        *        *     *        *     *        *
      AAC AAA CCT ATC ACT GTG TTG ACC CTC CAA TTA GAT GAC GAA TAT CGA
      Asn Lys Pro Ile Thr Val Leu Thr Leu Gln Leu Asp Asp Glu Tyr Arg>


         2550          2560          2570          2580          2590
       *     *     *        *     *     *        *     *      *        *
      CTA TAC TCT CCC CTA GTA AAG CCT GAT CAA AAT ATA CAA TTC TGG TTG
      Leu Tyr Ser Pro Leu Val Lys Pro Asp Gln Asn Ile Gln Phe Trp Leu>


            2600          2610          2620          2630
       *        *        *        *        *        *        *
      GAA CAG TTT CCC CAA GCC TGG GCA GAA ACC GCA GGG ATG GGT TTG GCA
      Glu Gln Phe Pro Gln Ala Trp Ala Glu Thr Ala Gly Met Gly Leu Ala>


   2640          2650          2660          2670          2680
    *        *        *     *        *        *        *        *        *
      AAG CAA GTT CCC CCA CAA GTT ATT CAA CTG AAG GCC AGT GCC ACA CCA
      Lys Gln Val Pro Pro Gln Val Ile Gln Leu Lys Ala Ser Ala Thr Pro>


   2690          2700          2710          2720          2730
    *        *        *        *        *        *     *        *        *     *
      GTG TCA GTC AGA CAG TAC CCC TTG AGT AAA GAA GCT CAA GAA GGA ATT
      Val Ser Val Arg Gln Tyr Pro Leu Ser Lys Glu Ala Gln Glu Gly Ile>


         2740          2750          2760          2770          2780
       *        *     *        *        *     *        *     *     *
      CGG CCG CAT GTC CAA AGA TTA ATC CAA CAG GGC ATC CTA GTT CCT GTC
      Arg Pro His Val Gln Arg Leu Ile Gln Gln Gly Ile Leu Val Pro Val>


            2790          2800          2810          2820          2830
       *        *     *        *     *        *        *     *     *        *
      CAA TCT CCC TGG AAT ACT CCC CTG CTA CCG GTT AGA AAG CCT GGG ACT
      Gln Ser Pro Trp Asn Thr Pro Leu Leu Pro Val Arg Lys Pro Gly Thr>


               2840          2850          2860          2870
          *        *     *        *     *        *     *        *        *
      AAT GAC TAT CGA CCA GTA CAG GAC TTG AGA GAG GTC AAT AAA CGG GTG
      Asn Asp Tyr Arg Pro Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val>


   2880          2890          2900          2910          2920
    *        *        *        *        *        *        *        *        *
      CAG GAT ATA CAC CCA ACA GTC CCG AAC CCT TAT AAC CTC TTG TGT GCT
      Gln Asp Ile His Pro Thr Val Pro Asn Pro Tyr Asn Leu Leu Cys Ala>


   2930          2940          2950          2960          2970
    *        *        *     *        *        *     *        *     *        *
      CTC CCA CCC CAA CGG AGC TGG TAT ACA GTA TTG GAC TTA AAG GAT GCC
      Leu Pro Pro Gln Arg Ser Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala>


      2980          2990          3000          3010          3020
       *        *        *        *        *        *        *        *     *
      TTC TTC TGC CTG AGA TTA CAC CCC ACT AGC CAA CCA CTT TTT GCC TTC
      Phe Phe Cys Leu Arg Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe>


         3030          3040          3050          3060          3070
       *        *     *        *        *     *        *        *     *        *
      GAA TGG AGA GAT CCA GGT ACG GGA AGA ACC GGG CAG CTC ACC TGG ACC
      Glu Trp Arg Asp Pro Gly Thr Gly Arg Thr Gly Gln Leu Thr Trp Thr>
```

FIGURE 3.CONT.

(SEQ ID NO: 3) cont'd

```
          3080        3090        3100        3110
           *     *     *     *    *    *     *     *     *
          CGA CTG CCC CAA GGG TTC AAG AAC TCC CCG ACC ATC TTT GAC GAA GCC
          Arg Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Ile Phe Asp Glu Ala>

     3120      3130        3140      3150        3160
      *     *     *     *    *    *     *     *     *     *
     CTA CAC AGA GAC CTG GCC AAC TTC AGG ATC CAA CAC CCT CAG GTG ACC
     Leu His Arg Asp Leu Ala Asn Phe Arg Ile Gln His Pro Gln Val Thr>

     3170        3180        3190      3200        3210
      *     *     *     *    *    *     *     *     *     *
     CTC CTC CAG TAC GTG GAT GAC CTG CTT CTG GCG GGA GCC ACC AAA CAG
     Leu Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Gly Ala Thr Lys Gln>

        3220        3230      3240        3250        3260
         *     *     *     *    *    *     *     *     *     *
        GAC TGC TTA GAA GGC ACG AAG GCA CTA CTG CTG GAA TTG TCT GAC CTA
        Asp Cys Leu Glu Gly Thr Lys Ala Leu Leu Leu Glu Leu Ser Asp Leu>

           3270        3280      3290        3300        3310
            *     *     *     *    *    *     *     *     *     *
           GGC TAC AGA GCC TCT GCT AAG AAG GCC CAG ATT TGC AGG AGA GAG GTA
           Gly Tyr Arg Ala Ser Ala Lys Lys Ala Gln Ile Cys Arg Arg Glu Val>

              3320        3330      3340        3350
               *     *     *     *    *    *     *     *     *
              ACA TAC TTG GGG TAC AGT TTG CGG GAC GGG CAG CGA TGG CTG ACG GAG
              Thr Tyr Leu Gly Tyr Ser Leu Arg Asp Gly Gln Arg Trp Leu Thr Glu>

     3360      3370        3380      3390        3400
      *     *     *     *    *    *     *     *     *     *
     GCA CGG AAG AAA ACT GTA GTC CAG ATA CCG GCC CCA ACC ACA GCC AAA
     Ala Arg Lys Lys Thr Val Val Gln Ile Pro Ala Pro Thr Thr Ala Lys>

       3410      3420        3430      3440        3450
        *     *     *     *    *    *     *     *     *     *
       CAA ATG AGA GAG TTT TTG GGG ACA GCT GGA TTT TGC AGA CTG TGG ATC
       Gln Met Arg Glu Phe Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile>

          3460        3470      3480        3490        3500
           *     *     *     *    *    *     *     *     *     *
           CCG GGG TTT GCG ACC TTA GCA GCC CCA CTC TAC CCG CTA ACC AAA GAA
           Pro Gly Phe Ala Thr Leu Ala Ala Pro Leu Tyr Pro Leu Thr Lys Glu>

              3510      3520        3530      3540        3550
               *     *     *     *    *    *     *     *     *     *
              AAA GGG GAA TTC TCC TGG GCT CCT GAG CAC CAG AAG GCA TTT GAT GCT
              Lys Gly Glu Phe Ser Trp Ala Pro Glu His Gln Lys Ala Phe Asp Ala>

                 3560        3570      3580        3590
                  *     *     *     *    *    *     *     *     *
                 ATC AAA AAG GCC CTG CTG AGC GCA CCT GCT CTG GCC CTC CCT GAC GTA
                 Ile Lys Lys Ala Leu Leu Ser Ala Pro Ala Leu Ala Leu Pro Asp Val>

     3600      3610        3620      3630        3640
      *     *     *     *    *    *     *     *     *     *
     ACT AAA CCC TTT ACC CTT TAT GTG GAT GAG CGT AAG GGA GTA GCC CGG
     Thr Lys Pro Phe Thr Leu Tyr Val Asp Glu Arg Lys Gly Val Ala Arg>
```

FIGURE 3, CONT.

(SEQ ID NO: 3) cont'd

```
     3650        3660        3670        3680          3690
      *      *     *     *     *      *     *      *      *    *
    GGA GTT TTA ACC CAA ACC CTA GGA CCA TGG AGA AGA CCT GTC GCC TAC
    Gly Val Leu Thr Gln Thr Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr>

          3700        3710        3720        3730        3740
           *      *     *      *     *     *      *      *     *
    CTG TCA AAG AAG CTC GAT CCT GTA GCC AGT GGT TGG CCC ATA TGC CTG
    Leu Ser Lys Lys Leu Asp Pro Val Ala Ser Gly Trp Pro Ile Cys Leu>

             3750        3760        3770        3780        3790
        *      *     *      *     *     *      *      *     *      *
    AAG GCT ATC GCA GCT GTG GCC ATA CTG GTC AAG GAC GCT GAC AAA TTG
    Lys Ala Ile Ala Ala Val Ala Ile Leu Val Lys Asp Ala Asp Lys Leu>

             3800        3810        3820        3830
        * ·    *      *     *     *      *     *      *     *
    ACT TTG GGA CAG AAT ATA ACT GTA ATA GCC CCC CAT GCA TTG GAG AAC
    Thr Leu Gly Gln Asn Ile Thr Val Ile Ala Pro His Ala Leu Glu Asn>

    3840        3850        3860        3870        3880
      *      *      *     *     *     *      *     *      *     *
    ATC GTT CGG CAG CCC CCA GAC CGA TGG ATG ACC AAC GCC CGC ATG ACC
    Ile Val Arg Gln Pro Pro Asp Arg Trp Met Thr Asn Ala Arg Met Thr>

    3890        3900        3910        3920        3930
      *      *      *     *     *      *     *      *     *·     *
    CAC TAT CAA AGC CTG CTT CTC ACA GAG AGG GTC ACG TTC GCT CCA CCA
    His Tyr Gln Ser Leu Leu Leu Thr Glu Arg Val Thr Phe Ala Pro Pro>

       3940        3950        3960        3970        3980
         *      *     *      *     *     *      *     *     *
    GCC GCT CTC AAC CCT GCC ACT CTT CTG CCT GAA GAG ACT GAT GAA CCA
    Ala Ala Leu Asn Pro Ala Thr Leu Leu Pro Glu Glu Thr Asp Glu Pro>

          3990        4000        4010        4020        4030
      *      *     *      *     *     *      *      *     *      ·*
    GTG ACT CAT GAT TGC CAT CAA CTA TTG ATT GAG GAG ACT GGG GTC CGC
    Val Thr His Asp Cys His Gln Leu Leu Ile Glu Glu Thr Gly Val Arg>

            4040        4050        4060        4070
         *      *  ·   *      *     *      *     *      *     *·
    AAG GAC CTT ACA GAC ATA CCG CTG ACT GGA GAA GTG CTA ACC TGG TTC
    Lys Asp Leu Thr Asp Ile Pro Leu Thr Gly Glu Val Leu Thr Trp Phe>

    4080        4090        4100        4110        4120
      *      *     *      *     *      *     *     *      *      *
    ACT GAC GGA AGC AGC TAT GTG GTG GAA GGT AAG AGG ATG GCT GGG GCG
    Thr Asp Gly Ser Ser Tyr Val Val Glu Gly Lys Arg Met Ala Gly Ala>

    4130        4140        4150        4160        4170
      *      *     *      *     *      *     *     *      *      *   *
    GCG GTG GTG GAC GGG ACC CGC ACG ATC TGG GCC AGC AGC CTG CCG GAA
    Ala Val Val Asp Gly Thr Arg Thr Ile Trp Ala Ser Ser Leu Pro Glu>

    4180        4190        4200        4210        4220
      ·   *      *     *      *     *      *     *      *     *     *
    GGA ACT TCA GCA CAA AAG GCT GAG CTC ATG GCC CTC ACG CAA GCT TTG
    Gly Thr Ser Ala Gln Lys Ala Glu Leu Met Ala Leu Thr Gln Ala Leu>
```

FIGURE 3, CONT.

(SEQ ID NO: 3) cont'd

```
        4230        4240        4250        4260        4270
     *     *     *     *     *     *     *     *     *     *
    CGG CTG GCC GAA GGG AAA TCC ATA AAC ATT TAT ACG GAC AGC AGG TAT
    Arg Leu Ala Glu Gly Lys Ser Ile Asn Ile Tyr Thr Asp Ser Arg Tyr>

           4280        4290        4300        4310
        *     *     *     *     *     *     *     *     *
    GCC TTT GCG ACT GCA CAC GTA CAT GGG GCC ATC TAT AAA CAA AGG GGG
    Ala Phe Ala Thr Ala His Val His Gly Ala Ile Tyr Lys Gln Arg Gly>

  4320        4330        4340        4350        4360
     *     *     *     *     *     *     *     *     *     *
    TTG CTT ACC TCA GCA GGG AGG GAA ATA AAG AAC AAA GAG GAA ATT CTA
    Leu Leu Thr Ser Ala Gly Arg Glu Ile Lys Asn Lys Glu Glu Ile Leu>

   4370        4380        4390        4400        4410
     *     *     *     *     *     *     *     *     *     *
    AGC CTA TTA GAA GCC GTA CAT TTA CCA AAA AGG CTA GCT ATT ATA CAC
    Ser Leu Leu Glu Ala Val His Leu Pro Lys Arg Leu Ala Ile Ile His>

     4420        4430        4440        4450        4460
        *     *     *     *     *     *     *     *     *
    TGT CCT GGA CAT CAG AAA GCT AAA GAT CTC ATA TCC AGA GGA AAC CAG
    Cys Pro Gly His Gln Lys Ala Lys Asp Leu Ile Ser Arg Gly Asn Gln>

        4470        4480        4490        4500        4510
     *     *     *     *     *     *     *     *     *     *
    ATG GCT GAC CGG GTT GCC AAG CAG GCA GCC CAG GGT GTT AAC CTT CTG
    Met Ala Asp Arg Val Ala Lys Gln Ala Ala Gln Gly Val Asn Leu Leu>

        4520        4530        4540        4550
     *     *     *     *     *     *     *     *     *
    CCT ATA ATA GAA ATG CCC AAA GCC CCA GAA CCC AGA CGA CAG TAC ACC
    Pro Ile Ile Glu Met Pro Lys Ala Pro Glu Pro Arg Arg Gln Tyr Thr>

  4560        4570        4580        4590        4600
     *     *     *     *     *     *     *     *     *     *
    CTA GAA GAC TGG CAA GAG ATA AAA AAG ATA GAC CAG TTC TCT GAG ACT
    Leu Glu Asp Trp Gln Glu Ile Lys Lys Ile Asp Gln Phe Ser Glu Thr>

  4610        4620        4630        4640        4650
     *     *     *     *     *     *     *     *     *     *
    CCG GAA GGG ACC TGC TAT ACC TCA GAT GGG AAG GAA ATC CTG CCC CAC
    Pro Glu Gly Thr Cys Tyr Thr Ser Asp Gly Lys Glu Ile Leu Pro His>

    4660        4670        4680        4690        4700
     *     *     *     *     *     *     *     *     *     *
    AAA GAA GGG TTA GAA TAT GTC CAA CAG ATA CAT CGT CTA ACC CAC CTA
    Lys Glu Gly Leu Glu Tyr Val Gln Gln Ile His Arg Leu Thr His Leu>

     4710        4720        4730        4740        4750
     *     *     *     *     *     *     *     *     *     *
    GGA ACT AAA CAC CTG CAG CAG TTG GTC AGA ACA TCC CCT TAT CAT GTT
    Gly Thr Lys His Leu Gln Gln Leu Val Arg Thr Ser Pro Tyr His Val>

        4760        4770        4780        4790
     *     *     *     *     *     *     *     *     *
    CTG AGG CTA CCA GGA GTG GCT GAC TCG GTG GTC AAA CAT TGT GTG CCC
    Leu Arg Leu Pro Gly Val Ala Asp Ser Val Val Lys His Cys Val Pro>
```

FIGURE 3, CONT.

```
      4800          4810          4820    ,      4830          4840          (SEQ ID NO: 3) cont'd
       *      *      *      *      *      *      *      *      *      *
      TGC CAG CTG GTT AAT GCT AAT CCT TCC AGA ATG CCT CCA GGG AAG AGA
      Cys Gln Leu Val Asn Ala Asn Pro Ser Arg Met Pro Pro Gly Lys Arg>


      4850          4860          4870          4880          4890
       *      *      *      *      *      *      *      *      *      *
      CTA AGG GGA AGC CAC CCA GGC GCT CAC TGG GAA GTG GAC TTC ACT GAG
      Leu Arg Gly Ser His Pro Gly Ala His Trp Glu Val Asp Phe Thr Glu>


         4900          4910          4920          4930          4940
          *      *      *      *      *      *      *      *      *
      GTA AAG CCG GCT AAA TAC GGA AAC AAA TAC CTA TTG GTT TTT GTA GAC
      Val Lys Pro Ala Lys Tyr Gly Asn Lys Tyr Leu Leu Val Phe Val Asp>


         4950          4960          4970          4980          4990
       *      *      *      *      *      *      *      *      *      *
      ACC TTT TCA GGA TGG GTA GAG GCT TAT CCT ACT AAG AAA GAG ACT TCA
      Thr Phe Ser Gly Trp Val Glu Ala Tyr Pro Thr Lys Lys Glu Thr Ser>


         5000          5010          5020          5030
       *      *      *      *      *      *      *      *      *
      ACC GTG GTG GCT AAA AAA ATA CTG GAA GAA ATT TTT CCA AGA TTT GGA
      Thr Val Val Ala Lys Lys Ile Leu Glu Glu Ile Phe Pro Arg Phe Gly>


     5040          5050          5060          5070          5080
       *      *      *      *      *      *      *      *      *      *
      ATA CCT AAG GTA ATA GGG TCA GAC AAT GGT CCA GCT TTT GTT GCC CAC
      Ile Pro Lys Val Ile Gly Ser Asp Asn Gly Pro Ala Phe Val Ala Gln>


     5090          5100          5110          5120          5130
       *      *      *      *      *      *      *      *      *      *
      GTA AGT CAG GGA CTG GCC AAG ATA TTG GGG ATT GAT TGG AAA CTG CAT
      Val Ser Gln Gly Leu Ala Lys Ile Leu Gly Ile Asp Trp Lys Leu His>


        5140          5150          5160          5170          5180
          *      *      *      *      *      *      *      *      *
      TGT GCA TAC AGA CCC CAA AGC TCA GGA CAG GTA GAG AGG ATG AAT AGA
      Cys Ala Tyr Arg Pro Gln Ser Ser Gly Gln Val Glu Arg Met Asn Arg>


        5190          5200          5210          5220          5230
       *      *      *      *      *      *      *      *      *      *
      ACC ATT AAA GAG ACC CTT ACT AAA TTG ACC GCG GAG ACT GGC GTT AAT
      Thr Ile Lys Glu Thr Leu Thr Lys Leu Thr Ala Glu Thr Gly Val Asn>


        5240          5250          5260          5270
       *      *      *      *      *      *      *      *      *
      GAT TGG ATA GCT CTC CTG CCC TTT GTG CTT TTT AGG GTT AGG AAC ACC
      Asp Trp Ile Ala Leu Leu Pro Phe Val Leu Phe Arg Val Arg Asn Thr>


     5280          5290          5300          5310          5320
       *      *      *      *      *      *      *      *      *      *
      CCT GGA CAG TTT GGG CTG ACC CCC TAT GAA TTA CTC TAC GGG GGA CCC
      Pro Gly Gln Phe Gly Leu Thr Pro Tyr Glu Leu Leu Tyr Gly Gly Pro>


     5330          5340          5350          5360          5370
       *      *      *      *      *      *      *      *      *      *
      CCC CCA TTG GTA GAA ATT GCT TCT GTA CAT AGT GCT GAC GTG CTG CTT
      Pro Pro Leu Val Glu Ile Ala Ser Val His Ser Ala Asp Val Leu Leu>
```

FIGURE 3, CONT.

```
          5380        5390        5400        5410        5420      (SEQ ID NO: 3) cont'd
           *       *    *       *       *    *       *    *    *
          TCC CAG CCT TTG TTC TCT AGG CTC AAG GCA CTT GAG TGG GTG AGA CAA
          Ser Gln Pro Leu Phe Ser Arg Leu Lys Ala Leu Glu Trp Val Arg Gln>

                5430        5440        5450        5460        5470
           *       *    *       *       *    *       *    *    *       *
          CGA GCG TGG AGG CAA CTC CGG GAG GCC TAC TCA GGA GGA GGA GAC TTG
          Arg Ala Trp Arg Gln Leu Arg Glu Ala Tyr Ser Gly Gly Gly Asp Leu>

                5480        5490        5500        5510
           *       *    *       *    *       *       *    *       *
          CAG ATC CCA CAT CGT TTC CAA GTG GGA GAT TCA GTC TAC GTT AGA CGC
          Gln Ile Pro His Arg Phe Gln Val Gly Asp Ser Val Tyr Val Arg Arg>

        5520        5530        5540        5550        5560
         *       *    *       *    *       *       *    *       *    *
          CAC CGT GCA GGA AAC CTC GAG ACT CGG TGG AAG GGC CCT TAT CTC GTA
          His Arg Ala Gly Asn Leu Glu Thr Arg Trp Lys Gly Pro Tyr Leu Val>

        5570        5580        5590        5600        5610
         *       *    *       *       *    *       *    *       *    *
          CTT TTG ACC ACA CCA ACG GCT GTG AAA GTC GAA GGA ATC TCC ACC TGG
          Leu Leu Thr Thr Pro Thr Ala Val Lys Val Glu Gly Ile Ser Thr Trp>

          5620        5630        5640        5650        5660
           *       *    *       *    *       *       *    *    *    *
          ATC CAT GCA TCC CAC GTT AAA CCG GCG CCA CCT CCC GAT TCG GGG TGG
              Met His Pro Thr Leu Asn Arg Arg His Leu Pro Ile Arg Gly Gly>

          Ile His Ala Ser His Val Lys Pro Ala Pro Pro Pro Asp Ser Gly Trp>

                5670        5680        5690        5700        5710
           *       *    *       *       *    *       *    *    *       *
          AAA GCC GAA AAG ACT GAA AAT CCC CTT AAG CTT CGC CTC CAT CGC GTG
          Lys Pro Lys Arg Leu Lys Ile Pro Leu Ser Phe Ala Ser Ile Ala Trp>

          Lys Ala Glu Lys Thr Glu Asn Pro Leu Lys Leu Arg Leu His Arg Val>

                5720        5730        5740        5750        5760
           *       *    *       *       *       *    *       *    *    *
          GTT CCT TAC TCT GTC AAT AAC CTC TCA GAC T AAT GGT ATG CGC ATA GGA
          Phe Leu Thr Leu Ser Ile Thr Ser Gln Thr   Asn Gly Met Arg Ile Gly>

          Val Pro Tyr Ser Val Asn Asn Leu Ser Asp>

                5770        5780        5790        5800
           *       *    *       *       *    *       *    *    *
          GAC AGC CTG AAC TCC CAT AAA CCC TTA TCT CTC ACC TGG TTA ATT ACT
          Asp Ser Leu Asn Ser His Lys Pro Leu Ser Leu Thr Trp Leu Ile Thr>

        5810        5820        5830        5840        5850
         *       *    *       *    *       *       *    *    *    +
          GAC TCC GGC ACA GGT ATT AAT ATC AAC AAC ACT CAA GGG GAG GCT CCT
          Asp Ser Gly Thr Gly Ile Asn Ile Asn Asn Thr Gln Gly Glu Ala Pro>
```

FIGURE 3,CONT.

```
        5860         5870         5880         5890         5900      (SEQ ID NO: 3) cont'd
         *      *      *      *      *      *      *      *      *
       TTA GGA ACC TGG TGG CCT GAT CTA TAC GTT TGC CTC AGA TCA GTT ATT
       Leu Gly Thr Trp Trp Pro Asp Leu Tyr Val Cys Leu Arg Ser Val Ile>

           5910         5920         5930         5940         5950
        *     *      *      *      *      *      *      *      *      *
       CCT AGT CTG ACC TCA CCC CCA GAT ATC CTC CAT GCT CAC GGA TTT TAT
       Pro Ser Leu Thr Ser Pro Pro Asp Ile Leu His Ala His Gly Phe Tyr>

              5960         5970         5980         5990         6000
            *      *      *      *      *      *      *      *      *      *
       GTT TGC CCA GGA CCA CCA AAT AAT GGA AAA CAT TGC GGA AAT CCC AGA
       Val Cys Pro Gly Pro Pro Asn Asn Gly Lys His Cys Gly Asn Pro Arg>

                   6010         6020         6030         6040
                 *      *      *      *      *      *      *      *      *
       GAT TTC TTT TGT AAA CAA TGG AAC TGT GTA ACC TCT AAT GAT GGA TAT
       Asp Phe Phe Cys Lys Gln Trp Asn Cys Val Thr Ser Asn Asp Gly Tyr>

       6050         6060         6070         6080         6090
         *      *      *      *      *      *      *      *      *      *
       TGG AAA TGG CCA ACC TCT CAG CAG GAT AGG GTA AGT TTT TCT TAT GTC
       Trp Lys Trp Pro Thr Ser Gln Gln Asp Arg Val Ser Phe Ser Tyr Val>

          6100         6110         6120         6130         6140
            *      *      *      *      *      *      *      *      *      *
       AAC ACC TAT ACC AGC TCT GGA CAA TTT AAT TAC CTG ACC TGG ATT AGA
       Asn Thr Tyr Thr Ser Ser Gly Gln Phe Asn Tyr Leu Thr Trp Ile Arg>

          6150         6160         6170         6180         6190
         *      *      *      *      *      *      *      *      *      *
       ACT GGA AGC CCC AAG TGC TCT CCT TCA GAC CTA GAT TAC CTA AAA ATA
       Thr Gly Ser Pro Lys Cys Ser Pro Ser Asp Leu Asp Tyr Leu Lys Ile>

             6200         6210         6220         6230         6240
           *      *      *      *      *      *      *      *      *      *
       AGT TTC ACT GAG AAA GGA AAA CAA GAA AAT ATC CTA AAA TGG GTA AAT
       Ser Phe Thr Glu Lys Gly Lys Gln Glu Asn Ile Leu Lys Trp Val Asn>

              6250         6260         6270         6280
            *      *      *      *      *      *      *      *      *
       GGT ATG TCT TGG GGA ATG GTA TAT TAT GGA GGC TCG GGT AAA CAA CCA
       Gly Met Ser Trp Gly Met Val Tyr Tyr Gly Gly Ser Gly Lys Gln Pro>

       6290         6300         6310         6320         6330
         *      *      *      *      *      *      *      *      *      *
       GGC TCC ATT CTA ACT ATT CGC CTC AAA ATA AAC CAG CTG GAG CCT CCA
       Gly Ser Ile Leu Thr Ile Arg Leu Lys Ile Asn Gln Leu Glu Pro Pro>

          6340         6350         6360         6370         6380
            *      *      *      *      *      *      *      *      *      *
       ATG GCT ATA GGA CCA AAT ACG GTC TTG ACG GGT CAA AGA CCC CCA ACC
       Met Ala Ile Gly Pro Asn Thr Val Leu Thr Gly Gln Arg Pro Pro Thr>

          6390         6400         6410         6420         6430
         *      *      *      *      *      *      *      *      *      *
       CAA GGA CCA GGA CCA TCC TCT AAC ATA ACT TCT GGA TCA GAC CCC ACT
       Gln Gly Pro Gly Pro Ser Ser Asn Ile Thr Ser Gly Ser Asp Pro Thr>
```

FIGURE 3, CONT.

(SEQ ID NO: 3) cont'd

```
           6440        6450        6460        6470        6480
        *     *     *     *     *     *     *     *     *     *
      GAG TCT AAC AGC ACG ACT AAA ATG GGG GCA AAA CTT TTT AGC CTC ATC
      Glu Ser Asn Ser Thr Thr Lys Met Gly Ala Lys Leu Phe Ser Leu Ile>


              6490        6500       ·6510        6520
        *     *     *     *     *     *     *     *     *
      CAG GGA GCT TTT CAA GCT CTT AAC TCC ACG ACT CCA GAG GCT ACC TCT
      Gln Gly Ala Phe Gln Ala Leu Asn Ser Thr Thr Pro Glu Ala Thr Ser>


     6530        6540        6550        6560        6570
        *     *     *     *     *     *     *     *     *     *
      TCT TGT TGG CTA TGC TTA GCT TCG GGC CCA CCT TAC TAT GAA GGA ATG
      Ser·Cys Trp Leu Cys Leu Ala Ser Gly Pro Pro Tyr Tyr Glu Gly Met>


          6580        6590        6600        6610        6620
        *     *     *     *     *     *     *     *     *.
      GCT AGA AGA GGG AAA TTC AAT GTG ACA AAA·GAA CAT AGA GAC CAA TGC
      Ala Arg Arg Gly Lys Phe Asn Val Thr Lys Glu His Arg Asp Gln Cys>


          6630·       6640        6650        6660       ·6670
        *     *     *     *     *     *     *     *     *     *
      ACA TGG GGA TCC CAA AAT AAG CTT ACC CTT ACT GAG GTT TCT GGA AAA
      Thr Trp Gly Ser Gln Asn Lys Leu Thr Leu Thr Glu Val Ser Gly Lys>


          .6680      . 6690        6700        6710        6720
        *     *     *     *     *     *     *     *     *     *
      GGC ACC TGC ATA GGA AAG GTT CCC CCA TCC CAC CAA CAC CTT TGT AAC
      Gly Thr Cys Ile Gly Lys Val Pro Pro Ser His Gln His Leu Cys Asn>


             6730        6740        6750        6760
        ·.    *     *     *     *     *     *     *     *   .
     .CAC ACT GAA GCC TTT AAT CAA ACC TCT GAG AGT CAA TAT CTG GTA CCT
      His Thr Glu Ala Phe Asn Gln Thr Ser Glu Ser Gln Tyr Leu Val Pro>


     6770        6780        6790        6800        6810
        *     *     *     *     *     *     *     *     *     *
      GGT TAT GAC AGG TGG TGG GCA TGT AAT ACT GGA TTA ACC CCT TGT GTT
      Gly Tyr Asp Arg Trp Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Val>


          6820        6830        6840        6850.       6860
        *     *     *     *     *     *     *     *     *     *
      TCC ACC TTG GTT TTT AAC CAA ACT AAA GAT TTT TGC ATT ATG GTC CAA
      Ser Thr Leu Val Phe Asn Gln Thr Lys Asp Phe Cys Ile Met Val Gln>


         . 6870        6880        6890       .6900        6910
        *     *     *     *     *     *     *     *     *     *
      ATT GTT CCC CGA GTG TAT TAC TAT CCC GAA AAA GCA ATC CTT GAT GAA
      Ile Val Pro Arg Val Tyr Tyr Tyr Pro Glu Lys Ala Ile Leu Asp Glu>


           6920        6930        6940        6950        6960
        *     *     *     *     *     *     *     *     *     *
      TAT GAC TAC AGA AAT CAT CGA CAA AAG AGA GAA CCC ATA TCT CTG ACA
      Tyr Asp Tyr Arg Asn His Arg Gln Lys Arg Glu Pro Ile Ser Leu Thr>


           6970        6980        6990    ·       7000
        *     *     *     *    ·*     *        *     *     *
      CTT GCT GTG ATG CTC GGA CTT GGA GTG GCA GCA GGT GTA GGA ACA GGA
      Leu Ala Val Met Leu Gly Leu Gly Val Ala Ala Gly Val Gly Thr Gly>
```

FIGURE 3.CONT.

(SEQ ID NO: 3) cont'd

```
        7010          7020          7030          7040          7050
     *        *    *        *    *        *        *    *    *        *
    ACA GCT GCC CTG GTC ACG GGA CCA CAG CAG CTA GAA ACA GGA CTT AGT
    Thr Ala Ala Leu Val Thr Gly Pro Gln Gln Leu Glu Thr Gly Leu Ser>

        7060          7070          7080          7090          7100
      *        *        *    *        *        *    *        *
    AAC CTA CAT CGA ATT GTA ACA GAA GAT CTC CAA GCC CTA GAA AAA TCT
    Asn Leu His Arg Ile Val Thr Glu Asp Leu Gln Ala Leu Glu Lys Ser>

        7110          7120          7130          7140          7150
    *        *        *    *        *        *    *        *        *
    GTC AGT AAC CTG GAG GAA TCC CTA ACC TCC TTA TCT GAA GTA GTC CTA
    Val Ser Asn Leu Glu Glu Ser Leu Thr Ser Leu Ser Glu Val Val Leu>

          7160          7170          7180          7190          7200
        *        *    *        *    *        *    *        *    *    *
    CAG AAT AGA AGA GGG TTA GAT TTA TTA TTT CTA AAA GAA GGA GGA TTA
    Gln Asn Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys Glu Gly Gly Leu>

              7210          7220          7230          7240
          *        *        *    *        *    *        *        *
    TGT GTA GCC TTG AAG GAG GAA TGC TGT TTT TAT GTG GAT CAT TCA GGG
    Cys Val Ala Leu Lys Glu Glu Cys Cys Phe Tyr Val Asp His Ser Gly>

     7250          7260          7270          7280          7290
       *        *    *        *    *    *        *        *    *        *
    GCC ATC AGA GAC TCC ATG AAC AAG CTT AGA GAA AGG TTG GAC AAG CGT
    Ala Ile Arg Asp Ser Met Asn Lys Leu Arg Glu Arg Leu Glu Lys Arg>

        7300          7310          7320          7330          7340
      *        *        *        *    *        *        *    *        *
    CGA AGG GAA AAG GAA ACT ACT CAA GGG TGG TTT GAG GGA TGG TTC AAC
    Arg Arg Glu Lys Glu Thr Thr Gln Gly Trp Phe Glu Gly Trp Phe Asn>

       7350          7360          7370          7380          7390
     *        *    *        *    *        *        *    *        *    *
    AGG TCT CTT TGG TTG GCT ACC CTA CTT TCT GCT TTA ACA GGA CCC TTA
    Arg Ser Leu Trp Leu Ala Thr Leu Leu Ser Ala Leu Thr Gly Pro Leu>

            7400          7410          7420          7430          7440
          *        *    *        *        *    *        *    *        *
    ATA GTC CTC CTC CTG TTA CTC ACA GTT GGG CCA TGT ATT ATT AAC AAG
    Ile Val Leu Leu Leu Leu Leu Thr Val Gly Pro Cys Ile Ile Asn Lys>

            7450          7460          7470          7480
          *        *    *        *    *        *    *        *    *
    TTA ATT GCC TTC ATT AGA GAA CGA ATA AGT GCA GTC CAG ATC ATG GTA
    Leu Ile Ala Phe Ile Arg Glu Arg Ile Ser Ala Val Gln Ile Met Val>

     7490          7500          7510          7520          7530
       *        *    *        *    *        *        *    *        *
    CTT AGA CAA CAG TAC CAA AGC CCG TCT AGC AGG GAA GCT GGC CGC
    Leu Arg Gln Gln Tyr Gln Ser Pro Ser Ser Arg Glu Ala Gly Arg>

          7540          7550          7560          7570          7580          7590
        *        *        *    *        *    *        *        *    *        *    *    *
    TAGCTCT ACCAGTTCTA AGATTAGAAC TATTAACAAG AGAAGAAGTG GGGAATGAAA
```

FIGURE 3, CONT.

          7600   7610   7620   7630   7640   7650   (SEQ ID NO: 3) cont'd
      *   *   *   *   *   *   *   *   *   *   *   *

      GGATGAAAAT   ACAACCTAAG   CTAATGAGAA   GCTTAAAATT   GTTCTGAATT   CCAGAGTTTG

          7660   7670   7680   7690   7700   7710
      *   *   *   *   *   *   *   *   *   *   *   *

      TTCCTTATAG   GTAAAAGATT   AGGTTTTTTG   CTGTTTTAAA   ATATGCGGAA   GTAAAATAGG

          7720   7730   7740   7750   7760   7770
      *   *   *   *   *   *   *   *   *   *   *   *

      CCCTGAGTAC   ATGTCTCTAG   GCATGAAACT   TCTTGAAACT   ATTTGAGATA   ACAAGAAAAG

          7780   7790   7800   7810   7820   7830
      *   *   *   *   *   *   *   *   *   *   *   *

      GGAGTTTCTA   ACTGCTTGTT   TAGCTTCTGT   AAAACTGGTT   GCGCCATAAA   GATGTTGAAA

          7840   7850   7860   7870   7880   7890
      *   *   *   *   *   *   *   *   *   *   *   *

      TGTTGATACA   CATATCTTGG   TGACAACATG   TCTCCCCCAC   CCCGAAACAT   GCGCAAATGT

          7900   7910   7920   7930   7940   7950
      *   *   *   *   *   *   *   *   *.   *   *   *

      GTAACTCTAA   AACAATTTAA   ATTAATTGGT   CCACGAAGCG   CGGGCTCTCG   AAGTTTTAAA

          7960   7970   7980   7990   8000   8010
      *   *   *   *   *   *   *   *   *   *   *   *

      TTGACTGGTT   TGTGATATTT   TGAAATGATT   GGTTTGTAAA   GCGCGGGCTT   TGTTGTGAAC

          8020   8030   8040   8050   8060   8070
      *   *   *   *   *   *   *   *   *   *   *   *

      CCCATAAAAG   CTGTCCCGAC   TCCACACTCG   GGGCCGCAGT   CCTCTACCCC   TGCGTGGTGT

          8080   8090   8100   8110   8120   8130
      *   *   *   *   *   *   *   *   *   *   *   *

      ACGACTGTGG   GCCCCAGCGC   GCTTGGAATA   AAAATCCTCT   TGCTGTTTGC   ATCAAAAAAA

      AA

FIGURE 3, CONT.